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March 31, 2004, 13:52:29; Search time 3483 Seconds (without alignments) 7167.840 Million cell updates/sec
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1 ATGAACGGAGGACGCCTT......ATGACGAGTAACTCCCCTCG 576
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		AR167456 Sequence	20001	ANTOSA / Segretare	AX740218 Sequence	BD096872 Isolated	BD218420 SSX gene,	U90841 Homo sapien	BC005325 HOMO BADI 54845 Semience 17	AX821947 Sequence	X86175 H.sapiens m	AR025465 Sequence	ARUBUSEU SEQUENCE	AR167453 Sequence	I85576 Sequence 2	AK287596 Sequence AR305668 Sequence	AX114023 Sequence	AX719099 Sequence	AX331558 Sequence	AX331950 Sequence	Z49105 H.Bapiens n 1190840 Homo sapien	BC016957 Homo sapi	BC007343 Homo sapi	S824/1 Homo sapre. AR167457 Sequence	AR170504 Sequence	AR182978 Seguence	AK3056/2 Sequence AX740219 Sequence	BD096873 Isolated	BD218421 SSX gene,	BC001003 Homo Sapi A48450 Sequence 15	U90842 Homo Bapien	52 Sequence	946	3416	X86174 H.Sapiens m BC016640 Homo sapi		linear PAT 17-DEC-2001				.o., old, L.J. and	cer in a sample by
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Gure, A.O., Tureci,O., Sahin, U., Tsang,S., Scanlan, M.J., Knuth, A.,
Gure, A.O., Tureci,O., Sahin, U., and Chen, Y.-T.
SSX family proteins
Patent: US 6339140-A 1 15-JAN-2002;
Location/Qualifiers
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Gure, A.O., Tureci,O., Sahin,U., Teang,S., Scanlan,M.J., Knuth,A.,
Ffreundschuh,M., Old,L.J. and Chen,Y.-T.
Isolated nucleic acid molecules encoding SSX family members and
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Best Local Similarity 100.0%; Pred. No. 2.6e-164;
Matches 576; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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Sequence 1 from patent US 6291658.
AR170503
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KHAWTHRLRERKQLVVYEEISDPEEDDE"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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Pfreundschuh,M., Old,L.J. and Chen,Y.T.
Isolated nucleic acid molecules encoding SSX family members
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1. .576
/organism="Homo sapiens"
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Sequence 1 from Patent.EP1300463.
AX740218 487740218.1 GI:30519358
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/db_xref="taxon:9606"
1. 576
/gene="SSX4"
1. 567
/gene="SSX4"
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         ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAAATATCAGAGAAG
                                          AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAAACTATGAGGTCATGACTAAA
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E. (bases 1 to 576)
S. Turedi,O., Sahin,U., Pfreundschuh,M., Rammensee,H.G. and Stevanovic,S.
Isolated peptides consisting of amino acid sequences four or NY-ESO-1 molecules, which bind to HLA molecules
Or NY-ESO-1 molecules, which bind to HLA molecules
Location/Qualifiers
1.576
1.576
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larity 100.0%; Pred. No. 2.6e-164;
Conservative 0; Mismatches 0;
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Sequence 5 from patent US 6548064.
AR305671
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Best Local Similarity
Matches 576; Conserv
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BDZ18420 SX gene, method of determining the occurrence of cancer in sample by determining the occurrence of cancer in sample by determining the expression of peptides originating in the SSX BDZ18420
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          members
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                 Topology: Linear;
Isolated nucleic acid molecules encoding SSX family
and uses
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                                                                   Location/Qualifiers
1. .576
/organism='Unidentified'
Location/Qualifiers
                                                                                                                                                                                                                                         100.0%; Score 576; DB 6; L
llarity 100.0%; Pred. No. 2.6e-164;
Conservative 0; Mismatches 0;
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                                                                                                                                            1. .576
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Strandedness: Single;
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JP 2002519013-A/5.
Homo sapiens (human)
Homo sapiens
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source
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Isolated mucleic acid molecules encoding SSX family members and uses thereof.
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25-DEC-2001
25-DEC-1994 D1 1998548050
05-MAY-1997 US 08/851138
ALI O GURE, CZLEM TURECI, UGUR SAHIN, SOLAM TSANG, MATTHEW J
                                                                                                                                     AATGGTTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAACAGCTGTGC
                                                                                 Argaacggaggcgcrrrrgcaaggagacccagggargargcrcaaaratcagagaag
                                                                                                                  CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
                                                  ATGAACGGAGGCCTTTGCAAGGAGCCCAGGGATGATGCTCAAATATCAGAGAAG
                   Gaps
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LUDMIG INSTITUTE FOR CANCER RESEARCH, MEMORIAL SLOAN
CANCER CENTER, CORNELL RESERCH FOUNDATION
OS Unidentified
                   Indels
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Gure, A.O., Tureci,O., Sahin,U., Tsang,S., Sca
Freundschuh,M., Old,L.J. and Chen, Y.T.
Isolated nucleic acid molecules encoding SSX
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   Pred. No. 2.6e-164;
Mismatches 0;
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BD096872.1 GI:22642460
JP 2001527408-A/1.
unidentified
   Local Similarity 100.0%; Pies 576; Conservative 0;
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420 420 480 480 540 540

Thu Apr

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/protein_id="AAC05820.1"
/db_xref="G1:2952023"
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SLQRIPPKIMPKKPABESENGIAKEVPPASGPQNDGKQLCPFGNPSTLEKINKTSGPKRG
KHAWTHRLRERKQLVVYEEISDPEEDDE"
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/gene="SSX4"
/gene="SSX4"
/note="corresponds to the 5' PCR primer that was used to isolate this gene and is identical to SSX2, GenBank Accession Number X86175; therefore, the SSX4 gene sequence might contain differences within this span"
                                                                                                                                                                                              PRI 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota, Metazoa; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 576)

Catarrhini; Hominidae; Homo.

(bases 1 to 576)

Catarrhini; Hominidae; Jager, E.,

Knuch, A., Tureci, O., Sahin, U., Tsang, S., Scanlan, M.J., Jager, E.,

Knuth, A., Pfreundschuh, M., Old, L.J. and Chen, Y.T.

SSX: a multigene family with several members transcribed in normal testis and human cancer

Int. J. Cancer 72 (6), 965-971 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cornell University, 1300
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/gene="SSX4"
/note="putative translation product; Kruppel-associated
box containing SSX gene"
/codon start=1
/product="SSX4"
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100.0%; Score 576; DB 9; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.6e-164;
Matches 576; Conservative 0; Mismatches 0; Indels
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                                 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
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mol_type="mRNA"
db_xref="taxon:9606"
1.576
gene="SSX4"
                                                                                                                                                                                                    576 bp
mRNA, c
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Homo sapiens SSX4 (SSX4)
U90841
U90841.1 GI:2952022
                                                                                                                                                                                                                                                                                                                                                    (human)
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   Tureci.O., Sahin, U., Pfreundschuh, M., Rammensee, G., Stevanovic, S., Chen, Y.T., Gure, M. and Caldi.J.

Tureci.O., Sahin, U., Defreundschuh, M., Rammensee, G., Stevanovic, S., Chen, Y.T., Gure, M. and Caldi.J.

Sax gene, method of determining the occurrence of cancer in sample by determining the expression of peptides originating in the SSX gene, method of determining the occurrence of cancer in sample by determining the expression of peptides originating in the SSX gene and NY-ESO-1 gene and utilization thereof.

Junking INSTITUTE FOR CANCER RESEARCH
OS Home sapiens (human)

Ph OZ-JUN-1999 JP 2000557145

PR 25-JUN-1999 JP 2000557145

PR 25-JUN-1999 US 09/105839

PR 25-JUN-1999 US 09/105839

PR 25-JUN-1999 US 09/105839

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les 576; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/codon_start=1
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              Email: cgapbs-remail.nih.gov
Tissue Produzement: ArCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Marx) mc@paxil.stanford.edu
Contact: (Dickson, Marx) mc@paxil.stanford.edu
Blickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: m Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28559011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCAGCAGAGGAAGAA
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/db_xref="CDD;smart00349"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/tissue_type="Bladder, carcinoma"
/clone lib="NH MGC_53"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.7%; Score 574.4; DB 9;
99.8%; Pred. No. 8.8e-164;
tive 0; Mismatches 1;
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59. 625
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I. (Bases 1 to 1250)
Strausberg, R.L., Feingold, E.A., Grouse, D.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Rah, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Schein, S., Ketteman, A., Montohman, J. McGren, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M. I., Skalska, U., Smallus, D.E.,
Schein, J.E., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC005325
Homo sapiens synovial sarcoma, X breakpoint 4, transcript variant
1, mRNA (cDNA clone MGC:12411 IMAGE:3961688), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (27 MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                             chadentropadencacconoccaccintrarecenacinamaacedecreeaerrocac
                                                                                                     GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
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1. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Proc. Natl. Acad. Sci.
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BC005325.1 GI:13529094
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                           512 ccccccccaaaaaccaacraccrcrcacaaaacaacaacccaaaaaccaa
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Method to modify differentiation of pluripotential stem cells
Patent: 10068961-A 75 21-AUG-2003;
Axordia Limited (696)-
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Pred. No. 4.6e-140;
0; Mismatches 49;
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1. 766
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                    Sequence 75 from Patent W003068961. AX821947
                                                                                                                                                                                                                                                                                                                         AX821947.1 GI:39725168
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Best Local Similarity 91.5%;
Matches 526; Conservative
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                                                               AAACATGCCTGGACCCACAGAGTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
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   TTCGGCAGCCTCCAGAGAATCTTCCCCGAAGATCATGCCCCAAGAAGCCAGCAGAGGAAGAA
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                                                                                               CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCCAAAAGGGGG
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Pred. No. 4.6e-140;
0; Mismatches 49;
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Cooper.C.S. and Gusterson, B.A.
MATERIALS AND METHODS RELATING TO THE DIMAND THERAPEUTIC TREATMENT OF SYNOVIAL SAL PALENT. WO 9602641-A 17 01-FEB-1996;
CANCER RES CAMPAIGN TECH (GB)
Other publication AU 2986595 960216.
Location/Qualitiers
Location/Qualitiers

1. 766
// Organism="unidentified"
// hol_type="unassigned" DNA"
// db_xref="taxon:32644"
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Sequence 17 from Patent W09602641.
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Pfreundschuh, M.

Pfreundschuh, M.

Stolated nucleic acid molecules which encode renal cancer specific antigens, and uses thereof

Patent: US 5798264-A 2 25-AUG-1998;

Location/Qualifiers
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                                           CTAGGITICAAGGCCACCTCCCACTTICATGTATAAACGGGCCGAAGACTTCCAG 331
                                                                                                              GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2 from patent US 5798264.
AR055465
AR025465.1 GI:3978093
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10-ce= "SSX2"

10-cedon Start=1

10-cedon 
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Cooper, C.S.
Cooper, C.S.
Submission
Submitted (lone, 1995) C.S. Cooper, Institute of Cancer Research,
Haddow Laboratories, Cotswold Road, Sutton, Surrey SM2 5NG, UK
Location/Qualifiers
1 organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="adult"
                               572 GAACATGCCTGGACCCACAGTGCGTGAGAGAAAACAGCTGGTGATTTATGAAGAGATC 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crew, A.J., Clark, J., Fisher, C., Gill, S., Grimer, R., Chand, A., Shipley, J., Gusterson, B.A. and Cooper, C.S. Fusion of SYT to two genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel-associated box in human synovial sarcoma EMBO J. 14 (10), 2333-2340 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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481 AAACAIGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
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                                                                                                                                                                                                                                                                                                  linear
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20. .61.
/gene="SSX2"
/note="Kruppel aacciated box homology"
                                                                                                           575
                                                                                                                                                       632 Agcgaccergaggaagargacgagraacreeere 666
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H.sapiens mRNA for SSX2 protein.
X86175.
SSX1 care. GI:829113
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Db 459 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGAGCTGTGC 518 Qy 421 CCCCGGGAAATCCAAGTACCTTGGAGAAGTTAACAAGAGACATCTGGACCCCAAAAGGGGG 480	481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCA 	Qy 541 AGGACCTGAGGAAGATGACGAGTAACTCCCCTC 575	RESULT 15 ARI17874 LOCUS ARI17874 BERINTIN Sequence 2 from patent US 6140464.	VERSION ARITHOLY.1 GI:14098780 KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE I (bases 1 to 931) AUTHORS Pfreundschuh,M. and Rammensee,HG. TITLE Nonapeptides that bind a Him-A2.1 molecule JOHNNAL Patent: US 6140464-A 2 31-OCT-2000; FEATURES SOURCE I. 9310	/organism="unknown" /mol_type="unassigned DNA" ltch 86.2%; Score 496.6;	Best Local Similarity 91.5%; Pred. No. 4.7e-140; Matches 526; Conservative 0; Mismatches 49; Indels 0; Gaps 0; Qy 1 ATGAACGAGACGACGTTTGCAAGGAGACCAGGGATGATGCTCAAATATCAGAGAAG 60	61 TTACGAAAAGGCCTTCGATGATATTGCCAAAAATACTTCTCTAAGAAAGGAGGGGGAAAAAGGTG 159 ATCCAAAAAGGCCTTCGATGATTGCCAAATACTTCTCTAAGGAAGG	OY 121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180	Qy 181 CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAACGGGGTGCACACTTCCAC 240	Qy 241 GGGAATGAITTTGGTAACGATCGAAGGAATCAGGTTGAACGTCCTCAGATGACT 300	by 301 TTCGGCAGCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAAGAAAAA 360	OY 361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420	OY 421 CCCCGGGGAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAGGGGG 480	OY 481 AAACATGCCTGGACCGCACAGACTGGGAGAAAGCAGCTGGTGGTTGTTATGAAGAGATC 540
339 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT 398 301 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAAGAA 360 199 TTCGGCAGCTCCAGGGAATCTCCCCGAAGATCATGCCCAAGAAGCCAGCAGAAGAAGGAAG	AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 42 	421 CCCCGGGGAAATCCAAGTACCTIGGAGAAGATTAACAAAACATTGGACCCAAAAGGGGG 480 	481 AAACATGCCTGGACCCACAGACTGGAGAAAGCAGCTGGTGGTTATGAACAGATC 540	639 Se AA ATA	ORGANISM Unknown. Unclassified. Unclassified. 1 (bases 1 to 931) AUTHORS Pfreundschuh, M. TITLE Hodgkin's disease associated molecules and uses thereof	ODCKNAL Fatent: US 5840588-A Z 24-NOV-1998; FEATURES Location/Qualifiers 1. 931 /organism="unknown" /mol_type="unassigned DNA"	ν ₁ γ	1 ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG 60 	61 TTACGAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGAAAGA	121 AAATCCTCGGAGAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180	181 CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240	241 GGGAATGATTTTGGTAACGATCGAAGGAATCAGGTTGAACGTCCTCAGATGACT 300 	301 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGGAGGAAGAA 360	361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420

579 GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC 638

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541 AGCGACCTGAGGAAGATGACGAGTAACTCCCCTC 575

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Search completed: March 31, 2004, 16:39:15 Job time : 3494 secs

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5599.456 Million cell updates/sec
                                                                                                                                                                  March 31, 2004, 13:52:29 ; Search time 437 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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576 1 ATGAACGGACGACGCCTT.....ATGACGAGTAACTCCCCTCG 576 Perfect score: Seguence:

3373863 seqs, 2124099041 residues IDENTITY_NUC Gapoxt 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

6747726

Post-processing: Minimum Match 0% Maximum Match 100% length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Listing first 45 summaries

1: genesequi980s:*
2: genesequi990s:*
3: genesequi000s:*
4: genesequi001as:*
5: genesequi01bs:* genesequ2002s:* genesequ2003as:* genesequ2003bs:* genesequ2003cs:* geneseqn2004s:* N_Geneseq_29Jan04:* 1:_geneseqn1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abk84472 Human cDN	8	Adc09598 SSX-4 cDN	Aav70060 Human SSX	Aat11780 Human X-c	DNA er	Aad54033 Human col	Abg83844 Human SSX		Add25523 Binding d	Aat47748 Melanoma	Aav04267 Melanoma	Abl64122 Breast ca	Abl63730 Breast ca	Aas80402 DNA encod	Aas80399 DNA encod	Aav70061 Human SSX	Aat11779 Human X-c	Aat11781 Human SYT	Aat11782 Human SYT	Aas80401 DNA encod	Aas80404 DNA encod
SUMMARIES	ID	ABK84472	ABQ83858		AAV70060	AAT11780	ABS73282	AAD54033	ABQ83844	ADC09570	ADD25523	AAT47748	AAV04267	ABL64122	ABL63730	AAS80402	AAS80399	AAV70061	AAT11779	AAT11781	AAT11782		AAS80404
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5 AAS91978 7 ADA71938 9 ADC32171 5 ABN33980		8 ADA10966 8 ACH04006 4 AAF27660		4 AAC91340 6 ABQ99153 6 ABA01156 9 ADC30277	5 AAH41224 1 AAK91889
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ALIGNMENTS

RESULT

Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephitis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; drohu; respiratory distress syndrome; inflammatory bowel disease; crohu; s disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy. Human cDNA differentially expressed in granulocytic cells #1043. ABK84472 standard; cDNA; 576 BP. (first entry) 14-AUG-2002 ABK84472; ABK84472

03-OCT-2001; 2001WO-US030821. 03-OCT-2000; 2000US-0237189P. WO200228999-A2. Homo sapiens. 11-APR-2002.

Vockley J; Yamaga S, Weissman SM, WPI; 2002-435328/46. Beazer-Barclay Y,

(GENE-) GENE LOGIC INC.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 1043; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by by Abh chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are

Abs73281 DNA encod

ABS73281

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20.4

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modulating (M2) GA by contacting GC with an agent that alters the cappelaid of at least one gene in Gs; (2) Screening (M3) for an agent cappale of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression confidence in a lergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of carbogen or sterile inflammatory disease, by detecting the level of carbogen or sterile inflammatory disease, by detecting the level of carbogen or sterile inflammatory disease, by detecting the level of carbogen or sterile inflammatory disease, by contacting a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene (s) from Gs in the tissue. M1 capponse in a subject, exposure of a subject to a pathogen or sterile inflammation in a tissue; M4 is useful for detecting an inflammation of a subject to a pathogen or sterile inflammatory disease, conditions in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, or cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially controved in gramulocytes. Note: The sequence data for this parent did one form part of the printed specification, but was obtained in cftp. with a parent directly from WIPO at
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The present invention describes an isolated epitope (I) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VO) comprising (I). (I) has cytostatic activity. VC is useful for treating an animal, by administering to an animal the vaccine or immunotherapeutic composition. WC is also useful for evaluating immunopenicity of a vaccine or immunotherapeutic composition, by administering VC to an HLA-transpenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (I) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises Eliseput analysis, confiniting dilution analysis, flow cytometry, in situ hybridisation and/or polymerase chain reaction (PCR). AB0838843 to AB083888 and ABP74128 to ABP74133 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epitope, vaccine, immunotherapeutic; cytostatic; immunogenicity;
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Best Local Similarity 100.0%; Pred. No. 9.3e-172; Matches 576; Conservative 0; Mismatches 0; Indels Conservative 0; Mismatches 0; Andels Conservative 0; Mismatches 0; Indels 0; Mismatches 0; Mismatche
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                                      541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
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07-NOV-2001; 2001US-0337017P.
07-MAR-2002; 2002US-0363210P.
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major histocompatibility complex class I; MHC class I; cancer;
immunisation; ss.
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07-NOV-2001; 2001US-0337017P.
07-MAR-2002; 2002US-0363210P.
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epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemotherapy.

Dischemotherapy or surgery. The composition is also useful for evaluating immunospanicity of a vaccine or immunotherapeutic compound. Multimeric MHC immunospanicity of a vaccine or immunotherapeutic compound. Multimeric MHC response, by performing the method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunisation step. Compositions of the invention are useful for diagnosing a disease. The current sequence represents an epitope of the invention with high affinity for MHC class I.
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                                                                                                                                                                                                                                                                                                                                                     Length 1250;
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100.0%; Pred. No. 1.4e-171;
ive 0; Mismatches 0;
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Matches 576
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481 AAACATGCCTGGACCCACAGAGTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
                                                                                                                                                                                                                                     Human; SSX2 gene; synovial sarcoma; X-chromosome; breakpoint-2; ornithine-delta-aminotransferase; OATL2 gene; Xp11.2; SSX1 gene; translocation; chromosome-18; 18q11.2; SYT gene; gene fusion; SYT-SSX2; fusion protein; primer; PCR; polymerase chain reaction; Smal; LpSI; probe; antibody; monoclonal antibody; humanised antibody; hybridisation; antitemour; recombinant vaccine; vaccinia virus; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing synovial sarcoma by detection of e.g. SYT and SSX1 sequences, based on X18 trans-location - by amplification of trans-location sequences or detection of the encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents the SSX2 gene (synovial sarcoma X-chromosome breakpoint-2). The gene is at the location of a breakpoint at Xp11.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -Region present in SYT-SSX2 fusion"
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/note= "Binds primer AAT11784"
                                                          541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
                               541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
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note= "Breakpoint for SYT
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377. .379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq:CGI,
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                                                                                                                                                                                                                                                                                                                              cancer; diagnosis; therapy; ss.
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                                                                                                                                                                                                             Human X-chromosome SSX2 cDNA.
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                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of a newly isolated human SSX4 cDNA clone. The CDNA was isolated from a human testicular cDNA by PCR amplification using primers (see AAV70062-63) based on the known SSX2 sequence. A SSX5 clone (see AAV70061) was also obtained. 2 Forms of SSX4 were identified. One of these lacked nucleotides 331-466 but was otherwise identical to the present SSX4 sequence and is described as an alternatively spliced form. SSX4 shares 89.4% homology to SSX1 on the nucleotide level and 79.3% at the amino acid level. The inventional additionally provides expression vectors, transferred cells that can be used to produce SSX proteins, and primers (see AAV70062-73) useful for determining expression of an SSX gene in a sample. The
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                                                                                                                                                                                                                               gene family members - useful for assaying for cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                               new SSX genes can be used to assay for cancers such as melanoma
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                                                                                                                                                             Knuth A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 574.4; DB 2; Length 576; Pred. No. 3e-171; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 576 BP; 188 A; 127 C; 149 G; 112 T; 0 U; 0 Other;
                                                                                                                                                             Scanlan MJ,
                                                                                                                                                          Sahin U, Tsang S,
LJ, Chen Y;
                                                                                                                                                                                                                                                            Claim 5; Page 12; 19pp; English.
                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
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                                                                                                    97US-00851138
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huh M, Old LJ,
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Matches 575; Conserva
                                                                                                                                                                                                      WPI; 1998~610379/51
                                                                                                                                                                         Pfreundschuh M,
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                   WO9850528-A1
                                             12-NOV-1998
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us-09-975-856-1.rng

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the translocation t (X;18) (p11.2;q11.2) found in human synovial sarcomas, involving joining of the SYT gene (AAT11778) on chromosome-18 at 18q11.2 to SSX2. The gene fusion is then transcribed to produce an SYT-SSX2 (AAT11781) fusion transcript and translated into a fusion protein. SSX2 may be distinguished from related sequence SSX1 (AAT11779) by digestion with Smar and LSPI. Parimer AAT11784 has been used in polymerase chain reaction amplification of SX2 sequences. Detection of the gene or its product in an abnormal location or as a fusion may be used in diagnosis of synovial sarcoma, using primers, probes, humanised antibodies, monoclonal antibodies, etc. Antisense oligonucleotides and antibodies may also be used therapeutically, and antitumour recombinant vaccines may be constructed e.g. in a vaccinia virus vector
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within an ornithine-delta-aminotransferase OATL2 region, associated with
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Pred. No. 1.5e-146;
0; Mismatches 49;
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I). Treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (MSP) or, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating concepanic fusion protein, treating cancerous cells containing fusion concepanic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP) 90 (e.g. protein isoform in a patient heterozygous for (II). The method is useful CC protein isoform in a patient heterozygous for (II). The method is useful (I ymphoma, chronic myeloid leukaemia (CML), ALL, ALL, ALL, ALL, and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewings sarcoma and carcinoma, Ewings sarcoma, rheadomy carcinoma, the method is also useful for treating viral carcinoma. This represents the DNA sequence of a chromosome aberration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90.
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HSP-90, rheumatoid arthritis, cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
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Chromosome aberration, oncogenic fusion protein, cancer, proliferative disease, cellular protein isoform, heat shock protein 90;

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Score 496.6; DB 7;
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ilarity 91.5%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for diagnosing colon cancer in a subject which comprises identifying colon cancer-associated polypeptides as antigens that elicit immune response in colon cancer. The method is useful for diagnosing, determining onset, progression, or regression of colon cancer in a subject, or for selecting a course of treatment of a subject having or suspected of having colon cancer. The colon cancer-associated polypeptides are useful as markers for diagnosing colon cancer, and for following the course of treatment of colon cancer. The present sequence is human colon cancer-associated polypeptide gene
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                                                                                                                                                                                        CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480
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                                                                                                                                                                                                                                                     481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
                                                               TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGAGCCAGCAGAAGAAAA
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   GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                            Trodgeadecreeaggaarereecegaagareargeeeaagaageeaggaagga
                                                                                                                             <u> AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, colon cancer-associated polypeptide, immune response, therapy, colon cancer, gene; ds.
                                 GGGBATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colon cancer-associated polypeptide gene, SSX-2.
                                                                                                                                                                                                                                                                                                                   AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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                                                                                                                                                                                                                                                                                                                                                             cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (I). (I) has cytostatic activity. VC is useful for treating an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunotherapeutic composition. VC is also useful for evaluating administering VC to an HiA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a Teal and evaluating immunogenicity to determining specific T cell frequency, by contacting T cells useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis, limiting dilution analysis, flow eyrometry, in situ hybridisation and/or polymerase chain reaction (FC). Ago33658 and ABP74128 to hybridisation of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated epitope (I) and an epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 CTAGGTTTCAAGGCCACCCTCCCACCTTTCATGTGTAATAAACGGGCCGAAGACTTCCAG
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                                                                                                                                 Novel epitopes useful as vaccines, comprises peptides or nucleic acid encoding the peptides, that are useful epitopes of target-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 86.2%; Score 496.6; DB 7; al Similarity 91.5%; Pred. No. 1.5e-146; 526; Conservative 0; Mismatches 49;
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                                                                                                                                                                                                                                                                      Claim 1; Page 148; 352pp; English.
                                WPI; 2003-067518/06
                                                                    P-PSDB; ABP74130
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The invention relates to an isolated epitope polypeptide that has high affinity for major histocompatibility complex (MHC) class I, and an epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemotherapy, biochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC cell frequency. This method is useful for determining specific T cell frequency. This method prior to and subsequent to an immunosition step. Compositions of the invention are useful for diagnosition and inhigh affinity for MHC class I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epitope having high affinity for major histocompatibility complex class is useful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTTAAGGAAAGATG
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                                                                                                                                                    cancer;
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                                                                                                                                Epitope; immunological; vaccine;
BP.
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2002US-0363210P.
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ADC09570 standard; cDNA; 766
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07-MAR-2002;
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Melanoma; tumour
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03-JAN-1996;
10-MAY-1996;
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           Query Match
Best Local S:
Matches 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody dependent cell-mediated cytótoxicity; ADCC; complement fixation; analignant condition; B-cell disorder; melanoma; cardinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
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CTAGGITICAAGGCCACCTCCCACCTTICAIGIAATAAACGGGCCGAAGACTICCAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                     GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT.
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                                         GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
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                                                                                                        AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                ds; Binding domain; immunoglobulin; fusion protein; cytostatic; antiathritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1;
                                                                                                                                                                                                                                                                                                                                                                            Binding domain-immunoglobulin fusion protein-associated DNA #46.
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2002US-00053530.
2002US-0385691P.
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antibody dependent ce
malignant condition;
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17-JAN-2002;
03-JUN-2002;
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Length 766;
                                                  Indels
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Score 496.6; DB 9;
Pred. No. 1.5e-146;
0; Mismatches 49;
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96US-00644116.
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Similarity 91.5%;
Sc. Conservative
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designated HOM-MEL 40. It was isolated using a novel method in which a designated HOM-MEL 40. It was isolated using a novel method in which a central library proped. From malignant melanoma and expressed in E. collicated to remove interfering binding partners. This involved contacting the sample with lysates of untransfected host cells and with host cells transformed with the same vector (phage lambda) used to make the CDNA library. The method, termed serological fishing, can be used to detect antigens in human tissues, esp. tumour cells, which are useful in the molecular diagnosis of diseases and/or for immunotherapy and gene therapy of infectious, autoimmune and malignant diseases (see also AAT4744-49). HOM-MEL 40 is expressed in 50% of melanomas, 20% of prostate cancers, 20% of present cancers, 20% of breast cancers, but not in normal tissue. HAA-A2 positive tumour cells present a nonomer (see also AAW09449-52) derived from HOM-MEL, suggesting that HOM-MEL 40 specific vaccines, useful in inducing
                                                                       Novel method of serological fishing - allows isolation of molecules (esp. antigens) associated with pathological conditions, e.g. Hodgkin's disease, cancer or auto:immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytotoxic T lymphocytes, are possible
                                                                                                                                                                                Claim 31; Page 29; 44pp; English
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marker; antigen; diagnosis; serological fishing; human;

Melanoma antigen clone HOM-MEL-40.

22-JUN-1998

AAV04267;

BP.

AAV04267 standard; cDNA; 931

RESULT 12 AAV04267

Gaps . 0 Length 931; Sequence 931 BP; 274 A; 207 C; 231 G; 219 T; 0 U; 0 Other; 49; Indels Query Match 86.2%; Score 496.6; DB 2; Best Local Similarity 91.5%; Pred. No. 1.6e-146; Matches 526; Conservative 0; Mismatches 49;

158 120 300 480 279 ciadgirircaaggccaccicccacciricargidaaraaaaggccgaagacriccag 338 99 ATGAACGAGACGACGCTTTGCAAGGAGAGCCCACGGTTGGTGCTCAAATACCAGAGAAG 219 AAAGCCTCGGAGAAATCTTCTATGTGTATATGAAGAGAAGTATGAGGCTATGACTAAA GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT TTCGGCAGCCTCCAGAGATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGGAAGAA Tregeradecreeaggaarereecgaagareargeecgaagaageagagga 459 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGAGCTGTGC CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCCAAAAGGGGG ceccessaaaaceaactacerersaaaaatreacaasaaareessa 181 AAACATGCCTGGACCCCACAGACTGCGTGAGAAAGCAGGTGGTGGTTTATGAAGAGTC 579 GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC 1 ATGAACGGAGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAGA 159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 339 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT **AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCCACAAAATGATGGGAAACAGCTGTGC** 399 181 241 361 519 121 301 421 δ 셤 d ò g g ò d à 원 ð d ò ò δ ò

398

458 420 518 638

AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC

541

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Clone HOW-WEL-40 was isolated from a human malignant melanoma cDNA library using a method, designated serological fishing, designed to library using a method, designated serological fishing, designed to identify immunoreactive markers of disease. In this method, cells characteristic of a disease are used to prepare a cDNA library for transformation of eukaryotic or prokaryotic cells, and the cells grown to prepare the library, but not transfected, to remove any components reactive with these cells, then the stripped sample is similarly treated with laysate of the library cells, so that specific components in the sample may bind to the expression protein. Proteins that form cimputates are identified as disease markers. In the case of HOM-MEL-40, the new melanoma associated antigen is strongly expressed in melanoma, but not healthy tissues. The deduced amino acid sequence includes 3 tumour-associated peptides (see AAW41587-89) that bind to HLA-A2.1. The serological fishing method was also used to identify a claimed marker (see AAV04262) of Hodgkin's disease
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Best Local Similarity 91.5%; Pred. No. 1.6e-146;
Matches 526; Conservative 0; Mismatches 49;
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HOM-MEL-40; ss.
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CTAGGTTTCAAGGCCACCTCCCACCTTTCATGTGTAATAAACGGGCCGAAGACTTCCAG 338
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stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
                                                                      399 TTCGGCAGGCTCCAGGGAATCTCCCCGAAGATCATGCCCAAGAAGCCAGCAGAAGAA
                                                                                                           AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGAGCTGTGC
                                                                                                                           CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                                         519 CCCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAGATCTGGACCCAAAAAGGGGG
                                                                                                                                                               481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTGTTATGAAGAGTTC
                                                                                                                                                                                579 GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC
                 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                       AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAAACAGCTGTGC
                                                                                                                                                                                                                                                                                                                      Breast cancer related gene sequence SEQ ID NO:2459.
                                                                                                                                                                                                  AGCGACCTGAGGAAGATGACGAGTAACTCCCCTC 575
                                                                                                                                                                                                                   639 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 673
                                                                                                                                                                                                                                                                ABL64122 standard; DNA; 1309 BP
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2000US-0234923P.
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2000US-0236032P
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                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     WO200194629-A2
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25-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-2000;
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25-SEP-2000;
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancrealic cancer, adenocarcinoma, carcinoma, cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG
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Pred. No. 1.9e-146;
0; Mismatches 49; Indels 0;
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Best Local Similarity 91.5%; Pre
Matches 526; Conservative 0;
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01-NOV-2000; 2000US-0245084P.
2000US-0236842P
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Weaver Z;
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                                     29-SEP-2000;
02-OCT-2000;
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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (given in ABL61664 comprises a sequence (S) selected from 847 sequences (given in ABL61664 comprises a sequence (S) selected from 847 sequences (given in ABL61664 comprises a sequence (S) selected from 847 sequences (given in ABL61664 cortivity and can be used in the incoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the adata ollected with respect to the anti-neoplastic agent. M1 can be used in the treatment of cancer such properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, aenocarinoma, carcinoma, cancer, infiltrating ductal cancer, infiltrating lobular cancer, sequence cancer, infiltrating ductal cancer, infiltrating lung, secondary papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG
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Pred. No. 1.9e-146;
0; Mismatches 49; Indels 0;
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28-SEP-2000; 2000US-0236109P.
29-SEP-2000; 2000US-0236842P.
29-SEP-2000; 2000US-0236842P.
29-SEP-2000; 2000US-0236842P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-023756P.
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237604P.
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01-NOV-2000; 2000US-0247608P.
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                                                                                                                                                                                                                                                                                                                            Weaver Z;
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Soppet DR,
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stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
                                                                                                                                                                                                                                                                   579 GAACATGCCTGGACCCACAGACTGCGTGAGAGAAAAACAGCTGGTGATTATGAAGAGATCTC
   GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
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                                339 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
                                                              TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGCAGAGGAAGAA
                                                                                                                          AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                                                   CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
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2000US-0236033P.
2000US-0236034P.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of siees expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                    GAACATGCCTGGACCCACAGACTGCGTGAGAGAAAACAGCTGGTGATTTATGAAGAGATC 638
GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
                                                            CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                          AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                          AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGAAAGAGCTGTGC
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                                                                                                                                                                                                                                                       481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
                                   TTCGGCAGCCTCCAGAGAATCTTCCCGAAGAAGATCATGCCCAAGAAGCCAGCAGCAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #16206.
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23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS80402 standard; cDNA; 921
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polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did ont appear in the printed specification, but was obtained in flow wipo.int/pub/published_pct_sequences
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.larity 91.3%; Pred. No. 1.6e-143;
Conservative 0; Mismatches 48;
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Search completed: Ma Job time : 441 secs

Sequence Sequence

9992, App 115, App 147, App 1647, App 1647, App 1697, App 1697, App 1697, App 1698, App 1699, App

Sequence Seq

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TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGAAGAA 360
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100.0%; Score 576; DB 3; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.7e-184;
Matches 576; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-105-839D-5
) Sequence 5, Application US/09105839D
) Patent No. 6287756
) Patent No. 6287756
) APPLICANT: Tureci, Ozlem
) APPLICANT: Gure, Yao-Teeng
APPLICANT: Gure, Ali
) APPLICANT: Gure, Ali
) APPLICANT: Gure, Ali
) APPLICANT: Gure, Ali
) TITLE OF INVENTION: Method for Determining Presence of ()
) TITLE OF INVENTION: Method for Determining Presence of ()
) TITLE PEFENENCE: LUD 5556
CURRENT APPLICATION NUMBER: US/09/105,839D
) CURRENT FILING DATE: 1998-06-26
) PRIOR FILING DATE: 1998-06-26
) RUNG APPLICATION NUMBER: US 08/851,130
) RUNGER OF SEQ ID NOS: 72
US-09-833-039A-1

US-08-232-976-3144

US-09-621-976-992

US-09-24-5318-5

US-09-24-5318-5

US-09-10-621-3120-147

US-09-10-557-14

US-09-10-557-14

US-09-621-976-1092

US-09-621-976-1092

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US-09-097-1092

US-09-097-1093

US-09-097-109-1092

US-09-621-976-2813

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US-09-621-976-109394-13471

US-09-489-039A-13471
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 TYPE: DNA ORGANISM: Homo sapiens
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   US-09-105-839D-5
 SEQ ID NO 5
LENGTH: 57
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Sequence 1
Sequence 1
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1 ATGAACGGAGACGACGCCTT.....ATGACGAGTAACTCCCCTCG
                                                                                                 March 31, 2004, 15:19:29 ; Search time 97 Seconds
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1: /cgg12_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-851-138C-1
US-09-344-040C-5
US-09-334-040C-5
US-09-392-714-16
US-09-392-714-16
US-08-952-714-16
US-08-952-714-16
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US-08-952-714-16
US-08-952-714-16
US-08-952-714-16
US-09-368-128B-2
US-09-958-128B-2
US-09-958-128B-2
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Maximum Match 100%
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Perfect score:
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APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Scanlan. Matthew J.; Knuth Alexander; Pfreundschuh, Michael; Old,
APPLICANT: Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Family
TITLE OF INVENTION: Family
TITLE OF INVENTION: Family
TITLE OF INVENTION: Ammbers And Uses Thereof
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                                                      121 AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAACTATGAGGTCATGACTAAA
                                                                                                               CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGGTGCAGACTTCCAC
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/851,138
APPLICATION NUMBER: 08/851,138
FILING DATE: 5-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: HANGON, NO. 6339140man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 752-5958
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 nucleotides
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/796,780
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-796-780-1; Sequence 1, Application US/09796780; Patent No. 6339140
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APPLICANT: Gure, Loyd J.; Knuth Alexander; Pfreundschuh, Michael; Old,
APPLICANT: Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX Family
TITLE OF INVENTION: Members And Uses Thereof
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGG 480
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,138C
FILING DATE: 5-May-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6291658man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 752-5958
INFORMATION FOR SEQ ID NO: 1;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08851138C
Patent No. 6291658
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Best Local Similarity 100.
Matches 576; Conservative
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STRANDEDNESS: sing
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US-09-833-039A-5

Sequence 5. Application US/09833039A

Patent No. 6673350

GENERAL INFORMATION:
APPLICANT: Threci, Ozlem
APPLICANT: Pfreudschuh, Michael
APPLICATION NUMBER: US/09/833,039A
CURRENT FILING DATE: 1099-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-26

NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 576
TYPEN APPLICATION NUMBER: US 09/105,839
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                                                                                                                                                 Indels
                                                                                                         Length
                                                                                                         Score 576; DB 4; I
Pred. No. 1.7e-184;
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                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 576; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-344-040C-5
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APPLICANT: Tureei, Ozlem
APPLICANT: Tureei, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Remensee, Hans Georg
APPLICANT: Remensee, Hans Georg
APPLICANT: Remensee, Hans Georg
APPLICANT: Revensee, Sefen
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
TITLE OF INVENTION: Gene, and Uses Thereof
TITLE OF INVENTION: UMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
CURRENT FILING DATE: 1999-66-26
PRIOR FILING DATE: 1998-66-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 5
LENGTH: 576
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                                                                                                                             Length 576;
                                                                                                                      Query Match
100.0%; Score 576; DB 4; Length 5'
Best Local Similarity 100.0%; Pred. No. 1.7e-184;
Matches 576; Conservative 0; Mismatches 0; Indels
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Patent No. 6548064
GENERAL INFORMATION:
. STRANDEDNESS: single ; TOPOLOGY: linear US-09-796-780-1
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                                                                   1 Angaacesasaceacecerriscaaesasaceaesesarearecreaaarareaeaae
                                                                                                                                           TTACGAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGAAGAGGGGGAAAAGATG
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             Pred. No. 1.7e-184; Mismatches 0;
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Patent No. 6686147
GENERAL INPORMATION:
100.08; 71.
             Similarity 100.
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CORGANISM: Homo sapiens
US-09-392-714-16
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US-09-392-714-16
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                                                                                       Gaps
                                                 Length 576;
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APPLICANT: Gure, Iloyd J.
APPLICANT: Old, Iloyd J.
TITLE OF INVENTION: Cancer Associated Antigens and Uses;
TITLE OF INVENTION: Therefor
FILE REFERENCE: 10461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER OF FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                   Indels
                                               100.0%; Score 576; DB 4; L
100.0%; Pred. No. 1.7e-184;
ive 0; Mismatches 0;
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                                                                                   Conservative
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ORGANISM: Homo sapiens
                                                             1 Similarity
576; Conserv
       US-09-833-039A-5
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                                           Query Match
Best Local S
Matches 576
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GENERAL LINCOMMAILOW

APPLICANT: Scandar, Matthew J.

APPLICANT: Gure, Ali O.

APPLICANT: Williamson, Barbara

APPLICANT: Chen, Yao-Teeng

APPLICANT: Chen, Yao-Teeng

APPLICANT: Chen, Yao-Teeng

TITLE OF INVENTION: Cancer Associated Antigens and Uses

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

CURRENT APPLICATION NUMBER: US/09/392,714A

CURRENT APPLICATION NUMBER: PCT/US98/14679

EARLIER FILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 16

LENGTH: 766
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Pred. No. 1.3e-157;
0; Mismatches 49;
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Best Local Similarity 91.5%;
Matches 526; Conservative
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Length 576;

4.

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576;

Score

100.00;

Query Match

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US-08-761-119-2
| Sequence 2, Application US/08761119
| Sequence 2, Application US/08761119
| Patent No. 5798264
| GENERAL INFORMATION:
| APPLICANT: Pitendedchuh, Michael
| TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
| TITLE OF INVENTION: And Molecules Identified Thereby
| NUMBER OF SEQUENCES: 3
| CORRESPONDENCE ADDRESS:
| ADDRESSED: Felfe & Lynch
| STREET: B05 Third Avenue
| CITY: New York City
| STATE: New York City
| STATE: New York City
| STATE: New York City
                                                                                                                                                                                                                                                                                                                                                   159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGAGTG
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                                                                                                                                                   Score 496.6; DB 1; Length 931;
Pred. No. 1.5e-157;
0; Mismatches 49; Indels 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb
COMPUTER: IEM
SEQUENCE CHARACTERISTICS:
LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                 Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative (
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                     linear
                                              ; TYPE: nucleic
; STRANDEDNESS:
; TOPOLOGY: lin
US-08-479-328-2
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Patent No. 5698396

GENERAL INFORMATION:
APPLICANT:
PITLE OF INVENTION: Method For Identified Thereby
ITILE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES:
ADDRESSE: Falfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STRIE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                           92 argaacggaggagggggrintggaagaggaggggggggggggggggggggaggaggagg
                                                                                     152 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGGAGGGAAAAAGATG
                                                                                                                                                                          121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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NAME: Hanson, No. 5598396man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 5410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Mordperfect
CURRENT APPLICATION DATA:
APPLICATION NOMER: US/08/479,328
FILING DATE: 07-UNB-1995
CLASSIFICATION: 435
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US-08-479-328-2
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159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
ZITY: New York
ZITY: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 86.2%; Score 496.6; DB 2; Best Local Similarity 91.5%; Pred. No. 1.5e-157; Matches 526; Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,128B
FILING DATE: 21-UNBE-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/644,116
FILING DATE: 10-MAY: 1996
FILING DATE: 10-MAY: 1996
PRIOR APPLICATION NUMBER: 08/580,980
FILING DATE: 03-DANURX: 1996
PRIOR APPLICATION NUMBER: 08/479,328
FILING DATE: 07-UDNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: HANBON, NO. 5840568man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hanson, No. 5840568man D. REGISTRATION NUMBER: 30,946
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TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LI
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-668-128B-2
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Patent No. 5840568
GENERAL INFORMATION:
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 496.6; DB 1;
Pred. No. 1.5e-157;
0; Mismatches 49;
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ER: LUD 5410.3
                                   FILING DATE: G-DECEMBER-1996
JGASSIFCCATION: 435
FILING DATE: G-DECEMBER-1996
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-UUNE-1995
ATTORNEY/AGENT: 1NFORMATION:
NAME: HANSON, NO. 5798264man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5410.
TELEPHONE: (212) 688-200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
US-08-761-119-2
                   APPLICATION NUMBER: US/08/761,119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative
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US-08-668-128B-2
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481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAAGCAGCTGGTGGTTTATGAAGAGATC 540
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159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
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TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: Method For Identified Thereby
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
ZIP: New York
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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PRICK APPLICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANUARY-1996
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-UNE-1995
ATTONNEY/AGENT INFORMATION:
NAME: Hanson, No. 6017716man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5410.1
TELECHONE: (212) 688-9200
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,625
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08959625
Patent No. 6017716
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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        CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAAGGGGG
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Patent No. 5864015

GENERAL INFORMATION:
PAPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York City
STREET: Now York
STREET: Now York
STREET: Diskette, 3.5 inch, 360 kb storage
COMPUTER: ISM
COMPUTER
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Pred. No. 1.5e-157;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                            541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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TYPE: nucleic acid
STRANDEDNESS: double-stranded
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Best Local Similarity 91.5%;
Matches 526; Conservative
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US-08-905-445-2
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                 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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PRIOR DATE:
ON JOHN BER:
PILING DATE:
ON JOHN BARY-1996
APPLICATION NUMBER:
OR JOHN BARS:
NAME:
HANSON, NO. 6020134man D.
REGISTRATION NUMBER:
NAME:
HANSON, NO. 6020134man D.
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORM
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US-08-580-980A-2
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APPLICANT:
APPLICANT:
TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfs & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
ZIP: 10022
                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                               Length 931;
                                                                                                                                                                                                                                                          49; Indels
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: ISM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,466
                                                                                                                                                                                        Score 496.6; DB 3;
Pred. No. 1.5e-157;
0; Mismatches 49;
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LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
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Patent No. 6020134
                                                                                                                                                                                            Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative
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US-09-008-466-2
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US-08-959-625-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AAATCCTCGGAGAAARTCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 AAAGCCTCGGAGAAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA 278
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    579 GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC
                                                                                                                                                                                 RESULT 15
US-09-053-463-2
US-09-053-453-2
US-09-053-453-2
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llarity 91.5%; Pred. No. 1.5e-157;
Conservative 0; Mismatches 49;
                                                                                                         639 AGCGACCTGAGGAAGATGACGAGTAACTCCCCTC 673
                                                                              541 AGCGACCTGAGGAAGATGACGAGTAACTCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 526; Conserva
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            Isolating A Molecule
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TITLE OF INVENTION: Method For Identifying Or Isolati
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STRIE: 805 Third Avenue
CITY: New York
ZIP: 10022
CCMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: 1BM
COMPUTER: 1BM
COMPUTER: 1BM
COMPUTER: 1BM
    Method For Identifying Or Isolat
And Molecules Identified Thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

86.2%; Score 496.6; DB 3;

Best Local Similarity 91.5%; Pred. No. 1.5e-157;

Matches 526; Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                  SCHWARE: Wordperfect
CURRENT APPLICATION DATA:
PPELICATION NUMBER: US/08/580,980A
FILING DATE: 03-JANUARY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-UNE-1995
ATTORNEY,AGENT INFORMATION:
NAME: HAIBOR, NO. 6025191man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5410.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 10 NO: 2
TELECOMMUNICATION SEG 10 NO: 2
SEQUENCE CHARACTERISTICS:
LINGTH: 931 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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US-08-580-980A-2
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339 GGGAATGATTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT 398
                                                                     TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGACCAGCAGCAGGAAGAA.360
                                                                                                    399 TICGGCAGGCTCCAGGGAATCTCCCCCGAAGATCATGCCCAAGAAGCCAGCAGAGAAGGAA 458
                                                                                                                                                         361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCCACAAAATGATGGAAACAGCTGTGC 420
                                                                                                                                                                                        459 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGAGCTGTGC 518
                                                                                                                                                                                                                                                  421 CCCCCGGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480
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Search completed: March 31, 2004, 17:26:48 Job time : 99 secs

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US-09-975-856-1
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Sequence 59, App
Sequence 13, Appl
Sequence 64, Appl
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 5, Appli
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Sequence 1392, Ap
Sequence 402, App
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Sequence 6, Appl:
Sequence 6, Appl:
                                                                                                                                  March 31, 2004, 16:39:19 ; Search time 389 Seconds (without alignments) 5512.734 Million cell updates/sec
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                                                                                                                                                                                                                                                      576
1 ATGAACGGAGACGACCTT.....ATGACGAGTAACTCCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

1. /cgn2_6/ptodata/1/pubpna/US07_pUBCOMB.seq:*
2. /cgn2_6/ptodata/1/pubpna/US07_pUBCOMB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
4. /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5. /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6. /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
7. /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
8. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
10. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11. /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
12. /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
13. /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
14. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
15. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
16. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
17. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
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19. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
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12. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
13. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
14. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
15. /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-833-039-5
US-10-117-937-599
US-10-117-937-599
US-10-207-655-84
US-10-207-655-84
US-10-117-937-6
US-09-833-039-2
US-09-954-531-1000
US-09-954-531-1000
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US-09-975-856-2
US-09-833-039-6
US-10-177-277-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                               Title:
Perfect so
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                       Run on:
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No.
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	equence 1, Appl	equence 106782,	equence 24594,	equence 10234,	equence 235	eguence 33096,	97,	equence 148	Ō	equence 114	equence 114	325	equence 323	equence 1	4	quence 84, A	equence 5849	equence 5849	261,	equence 1347	equence 1896	equence 1896	equence 7375	2178	equence 1253	equence 181,	ednenc	ednence 38,	m
-08-833-038-	10-177-277-1	-10-027-632-1067	-10-027-632-2459	-10-029-386-1023	-10-029-386-2395	-10-027-632-3309	-10-027-632-3309	-10-027-632-14878	S-10-027-6	10-027-632-11451	-10-027-632-11451	-10-027-632-32243	-10-027-632-32243	-09-814-353-1848	3-09-908-975-672	19-981-353-84	3-10-085-783A-58	3-10-242-535A-58	10-133-013-261	-10-027-632-13477	-10-085-783A-18	-10-242-535A-1896	-10-029-386-737	09-814-353-2178	-10-108-260A-1	-10-098-841-181		-09-971-392-98	7-632-1
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Sequence 1, Application US/09975856
Publication No. US20030023057A1
GENERAL INFORMATION:
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Gare, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
ZIP: 10103
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hanson, No. UG20030023057Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                        Members And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 1BM
OPERATION SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/975,856
FILING DATE: 11.0ct-2001
CLASSIFICATION: <UNKNOWN>
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION WUMBER: 09/796,780
FILING DATE: 2001-03-01
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 31
TELEFAX: (212) 752-
INFORMATION FOR SEQ ID NO: 1:
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NOS: 129
              SEQ ID NO 5
LENGTH: 576
TYPE: DNA
CRGANLSM: HOMO Sapiens
US-09-833-039-5
                                                                                                                  Query Match
Best Local Similarity
Matches 576; Conserv
 NUMBER OF SEQ ID
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Sequence 5, Application US/09833039

Publication No. US20030175960A1

GENERAL INFORMATION:

APPLICANT: Tureci, Ozlem

APPLICANT: Sahin, Ugur

TITLE OF INVENTION: Tureci Associated Peptide and Uses Thereof

TITLE OF INVENTION: Tureci 2001-04-12

FRIER REFERENCE: LUD 5622.1

CURRENT APPLICATION NUMBER: US 09/409,455

PRIOR FLIING DATE: 1999-03-30

PRIOR PELICATION NUMBER: US 09/400

PRIOR PELICATION NUMBER: US 09/344,040

PRIOR FILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                     ;
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                                                                                                                                    Length 576;
                                                                                                                                                                     Indels
                                                                                                                                   100.0%; Score 576; DB 10; 100.0%; Pred. No. 2.8e-174;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   Conservative
                                                                                                                               Query Match
Best Local Similarity
Matches 576; Conserva
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Length 576;
100.0%; Score 576; DB 10;
.larity 100.0%; Pred. No. 2.8e-174;
Conservative 0; Mismatches 0;
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                                                                                                                                                                      Score 576; DB 15;
Pred. No. 2.8e-174;
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Sequence 13, Application US/09849602
Publication No. USZ0030165834A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stanlan, Matthew J.
APPLICANT: Stanlan, Yao-Tsebeth
APPLICANT: Chen, Yao-Tsebeth
APPLICANT: Chen, Yao-Tsepen
PILE REFERENCE: L0461/7105(JRV)
CURRENT APPLICATION: Colon Cancer
FILE REPERENCE: L0461/7105(JRV)
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 766
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                                                                                                                                                                   Query Match
100.0%; Score 576; D
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 576; Conservative 0; Mismatches
  NUMBER OF SEQ ID NOS: 602
SOFTWARE: RestSEQ for Windows Version 4.0
SEQ ID NO 599
LENGTH: 576
                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-117-937-599
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CORGANISM: Homo sapien
US-09-849-602-13
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                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                          Length 576;
                                                                                                                                                                                                                0; Indels
                                                                                                                                                                        Score 576; DB 14;
Pred. No. 2.8e-174;
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100.0%; Pred. No. c...
0; Mismatches
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APPLICANT: SIMARD, John, J.L.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIJAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REPERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-10-7
PRIOR FILING DATE: 2001-11-7
PRIOR FILING DATE: 2001-10-7
PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 599, Application US/10117937; Publication No. US20030220239A1; GENERAL INFORMATION:
; PRIOR FILING DATE: 1997-05-05; NUMBER OF SEQ ID NOS: 132; SEQ ID NO 5; LENGTH: 576; TYPE: DNA; CORGANISM: HOMO Sapiens US-10-177-277-5
                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 576; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-117-937-599
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92 ATGAACGGAGACGACGCTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG 151
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                                                                                                                     AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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86.2%; Score 496.6; DB 15;
Best Local Similarity 91.5%; Pred. No. 1e-148;
Matches 526; Conservative 0; Mismatches 49;
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Sequence 6, Application US/10117937
PUDLICATION NO. US2003022029A1
GENERAL INFORMATION:
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAWOND, David, C.
APPLICANT: LIU, Liphing
APPLICANT: LIU, Liphing
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-01-07
PRIOR PLING DATE: 2001-11-07
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; ORGANISM: Homo sapiens
US-10-117-937-6
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CURRENY APPLICANTON NUMBER: US/10/207,655
CURRENY FILING DATE: 2022-07-25
NUMBER OF SEQ ID NOS: 2022-07-25
SOFTWARE PATENT OF SEQ ID NOS: 2022-07-25
SEQ ID NO 84
LENGTH: 766
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                              Length 766;
                              Query Match
Best Local Similarity 91.5%; Pred. No. 1e-148;
Matches 526; Conservative 0; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative
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CORGANISM: Homo sapiens
US-10-207-655-84
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US-10-207-655-84
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Sequence 2, Application US/1017277

| Sequence 2, Application US/1017277
| Publication No. US20030185844A1
| GENERAL INFORMATION:
| APPLICANT: Tureci, Ozlem
| APPLICANT: Sahin, Ugur
| APPLICANT: Ramensee, Hans Georg
| APPLICANT: Ramensee, Hans Georg
| APPLICANT: Stevanovic, Stefan
| TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determ
| TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
| TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
| TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
| TITLE OF INVENTION: UNMER: US/10/177,277
| CURRENT APPLICATION NUMBER: US 09/105,839
| FRIOR APPLICATION NUMBER: US 09/105,839
| PRIOR FILING DATE: 1999-06-26
| PRIOR FILING DATE: 1999-06-26
| PRIOR FILING DATE: 1999-06-26
| PRIOR FILING DATE: 1990-06-26
| PRIOR FILING
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                                                                                                                                                                                                                                                                                                                                                        241 GGGAATGATTTTGGTAACGATCGAAACCAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                        arccaaaaggccrrcgargararrgccaaaracrrcrcraaggaagagrggaaaaa
                                                                                                                                                AAAGCCTCGGAGAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA
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Pred. No. 1.1e-148;
0; Mismatches 49;
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Best Local Similarity 91.5%;
Matches 526; Conservative
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152 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG
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Publication No. US20030175960A1

GENERAL INFORMATION:

APPLICANT: Turcei, Ozlam

APPLICANT: Sahin, Ugur

APPLICANT: Pfreundschuh, Michael

TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof

TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/833,039

CURRENT APPLICATION NUMBER: US 09/409,455

PRIOR APPLICATION NUMBER: US 09/409,455

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: US 09/105,839

PRIOR APPLICATION NUMBER: US 09/105,839

PRIOR APPLICATION NUMBER: US 08/851,130

PRIOR PILING DATE: 1997-06-05

PRIOR PILING DATE: 1997-06-05

PRIOR FILING DATE: 1997-06-05

NUMBER OF SEQ ID NOS: 129
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CRGANISM: Homo sapiens
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Sequence 1992, Application US/09954531
Parent No. US20020165180A1
GENERAL INPORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Carleta Delivery Meaver.
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Carleta Delivery Meaver.
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689200-77
CURRENT FILING DATE: 2002-05-02
PRIOR PAPLICATION NUMBER: US/60/234,009
PRIOR PILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-22
PRIOR PRILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: Patentin version 3.0
SEQ ID NO 1392
LENGTH: 1309
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NAME/KRY: misc_feature
NCATLON: (1): (1309)
OTHER INFORMATION: n=a,t,g or
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TITLE OF INVENTION: Gene Sets

FILE REPRENCE: 68290-77

CURRENT FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR FILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SOFFWARE: Patentin version 3.0

SEQ ID NO 1000
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GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
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                                      <u> ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG</u>
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Pred. No. 1.4e-148;
0; Mismatches 49;
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                                                                                                                                                         CTAGGTTTCAAGGTCACCCTCCCACC
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Best Local Similarity 91.5%;
Matches 526; Conservative
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Sequence 2, Application US/09975856
Publication No. US20020023057A1
GENERAL INFORMATION:
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT Gran, Matchew J.; Knuth Alexander; Pfreundschuh, Michael; Old, Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb
COMFUTER: IBM
OPERATING SYSTEM: PC-DOS
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ADDRESSEE: Whibright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
  Mismatches
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FILING DATE: 11-Oct-2001
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 09/796,780
FILING DATE: 2001-03-01
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ZIP: 10103
  Conservative
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Bublication No. US20040009154A1

Bublication No. US20040009154A1

Bublication No. US20040009154A1

APPLICANT: Khan, Javed

APPLICANT: Ringner, Markus

APPLICANT: Ringner, Markus

APPLICANT: Ringner, Markus

APPLICANT: Ringner, Paul

TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS

TILE REFERENCE: 11613-56USII

CURRENT APPLICATION NUMBER: US/10/159,563
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                                          Length 1309;
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                                                                                   Indels
                                        Score 496.6; DB 9;
Pred. No. 1.4e-148;
0; Mismatches 49;
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Pred. No. 2.1e-148;
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PRIOR FILMS DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: Patentin version 3.1
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91.3%;
                                        h 86.2%;
Similarity 91.5%;
26; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
  US-09-954-531-1392
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US-10-159-563-402
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PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR PILING DATE: 1999-06-26
PRIOR PILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 6
                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.9%;
Matches 517; Conservative
                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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US-10-177-277-6
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US-09-833-039-6
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Pred. No. 3.7e-144;
0; Mismatches 58; Indels
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Publication No. US20030175960A1
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Tureci, Ozlem
APPLICANT: Shin, Ugur
APPLICANT: Pfreundschuh, Michael
ITLE OF INVENTION: Tumor Associated Peptide and
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
               NAME: Hanson, No. US20030023057Alman
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5480
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                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
ORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 nucleotides
                                                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: US-09-975-856-2
   ATTORNEY/AGENT INFORMATION
                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 89.9%;
Matches 517; Conservative
                                                                                                    INFORMATION
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Sequence 6, Application US/1017277
Publication No. US203010185844A1
GENERAL INFORMATION:
APPLICANT: Tured, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determ
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene;
TITLE OF INVENTION: Gene, and Uses Thereof
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Length 576;
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DB 10;
Score 482.2; DB 10;
Pred. No. 3.7e-144;
0; Mismatches 58;
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89.9%; Pred. No. 3.7e-144;
cive 0; Mismatches 58; Indels 0;
CURRENT APPLICATION NUMBER: US/10/177,277
CURRENT FILING DATE: 2002-06-21
FRICA APPLICATION NUMBER: US/09/344,040
FRICA FILING DATE: 1999-06-25
FRICA APPLICATION NUMBER: US 09/105,839
FRICA FILING DATE: 1998-06-26
FRICA APPLICATION NUMBER: US 08/851,130
FRICA RILING DATE: 1998-06-26
FRICA APPLICATION NUMBER: US 08/851,130
FRICA FILING DATE: 1997-05-05
SEQ ID NO 6: SEQ ID NOS: 132
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Best Local Similarity 89.9°
Matches 517; Conservative
                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-277-6
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYMBL utstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 161 LysHisAlaTrpThrHisArgLeuArgGluArgLysGlnLeuValValTyrGluGlulle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96302330; PubMed=8697803; de Leeuw B., Balemans M., Geurts van Kessel A.; Lalemans M., Geurts van Kessel A.; Kruppel-associated box containing the SSX gene (SSX3) on the human X chromosome is not implicated in t(X,18)-positive synovial
                                                    AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTTATGAAGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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368C7487C1450E72 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR001909; KRAB.
InterPro; IPR003655; KRAB_related.
Pfam; PP01352; KRAB; 1.
SWART; SM00349; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Fibrosarcoma, and Testis;
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"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                       Menzel
                                                                 SECUENCE OF 1-155 FROM N.A.
Blechschmidt K., Nyakatura G., Strom T.M., Drescher B., I Meindl A., Rosenthal A.;
Submitted (CT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Could act as a modulator of transcription.
-!- SIMILARITY: Belongs to the SSX family.
-!- SIMILARITY: Contains 1 KRAB-related domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4ACA2A8737507AE5 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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InterPro; IPR003655; KRAB_related.
PEam; PF00352; KRAB; 1.
SMART; SM00349; KRAB; 1.
PR0STIE; PS50806; KRAB RELATED; 1.
DOMSTIE; PS50806; KRAB RELATED; 1.
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EMBL; BC05325; AAH05325.1; --.
EMBL; AF196972; AAF06796.1; --.
Genew; HGNC:11338; SSX4.
MIM; 300326; --.
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SEQUENCE 188 AA; 21858 MW;
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                                      ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG
                                                                                       AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
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MEDLINE=9529294; PubMed=7539744;

Crew A.J., Clark J., Fisher C., Gill S., Grimer R., Chand A.,
Shipley J., Gusterson B.A., Cooper C.S.;

"Rusion of SYT to two genes, SSX1 and SSX2, encoding proteins with
homology to the Kruppel-associated box in human synovial sarcoma.";

EMBO J. 14:2333-2340(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.L., Feingold E.A., Grouse b.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        SSXZ HUMAN STANDARD; PRT, 188 AA.
Q163<u>B</u>5, Q16404; Q961P7;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
11-OCT-2003 (Rel. 42, Last annotation update)
SSXZ protein (Synovial sarcoma, X breakpoint 2) (SSX) (HOM-MEL-40)
SSXZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Gaps:
                   US-09-975-856-1 (1-576) x SSX3 HUMAN (1-188)
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Repokins R.F. Corden H. W. Farmer A.A. S. I. Wands U. Heide P., R. Stepleton W. Soares W. B. Fording M. Woore T. W. Soares W. B. Stepleton W. Soares W. B. Fording M. Wool U. Carminol P. Pernog C. S. Bromalow R. C. Walland W. Soares W. B. S. Locklon W. B. Fording M. S. Carminol P. Pernog C. S. Bromalow R. C. Walland W. S. Soares W. S. Bonalow R. C. Walland W. S. S. W. Woone M. C. Carminol P. S. Walland W. S. W. Woone M. C. Walland M. S. Walland W. S. W. Woone M. C. Walland M. Wall
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10-OCT-2003 (Rel. 42, L
SSX1 protein (Synovial
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         30, GO:0006355; P:regulation of transcription, DNA-dependent; NAS
                                                                                  BREAKPOINT FOR TRANSLOCATION TO SSXT-SSX2 FUSION PROTEIN (RARE). BREAKPOINT FOR TRANSLOCATION TO SSXT-SSX2 FUSION PROTEIN. R -> P (IN REF. 2; AAH07343). BF5D18AA5P45B1B1 CRC64;
               InterPro; IPR001999; KRAB.
InterPro; IPR001655; KRAB_related.
Pfam; PF0152; KRAB; 1.
PROSITE; PS50806; KRAB; 1.
Chromosomal translocation; Proto-oncogene; Multigene family;
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SSX1 HUMAN
ID SSX1 HUMAN
AC Q16384;
DT 15-DEC-1998 (
DT 15-DEC-1998 (
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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RX MEDINE=2238825; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Blacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Robas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S.S., Worley K.C., McKernan K.J., Malek J.A., Gubzartne P.H.,

RA Richards S.W., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Halton E., Retteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mitting M., Madan A., Young A.C., Schwutz J., Myers R.M.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Samilus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. "Generation and initial analysis of more than 15,000 full-length
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MEDLINE=95384157; PubMed=7655467;
Me Leeuw B., Balemans M., Olde Weghuis D., Geurts van Kessel A.;
de Leeuw B., Balemans M., Olde Weghuis D., Geurts van Kessel A.;
If dentification of two alternative fusion genes, SYT-SSX1 and
SYT-SSX2, in t(X.18) [pl.1.2]-posltive synovial sarcomas.";
If Hum. Mol. Genet. 4:1097-1099(1995).
I TISSUB SPECIFICITY: Expressed at high level in the testis.
Expressed at low level in thyroid. Not detected in tonail, colon, lung, spleen, prostate, kidney, striated and smooth muscles.
Detected in rhabdomyosarcoma and fibrosarcoma cell lines. Not detected in mesenchymal and epithelial cell lines.
Colon better detected in mesenchymal and epithelial cell lines.
Colon better detected in the specifically found in more than 80% of translocation that is specifically found in more than 80% of synovial sarroma and produces the SSXT-SSXI or SSXT-SSXI or SSXT-SSXI fusion products. These hybrid processor sprobably responsible for transforming activity, Heterogeneity in the position of the brashpoint can occur (low frequency).

L'SIMILARITY: Belongs to the SSX family.
Colon SIMILARITY: Contains 1 KRAB-related domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fibrosarcoma;

MEDLINE-25929374, pubmed=7539744;

Crew A.J., Clark J., Fisher C., Gill S., Grimer R., Chand A.,
Shipley J., Gusterson B.A., Cooper C.S.;
Fibilon of SYT to two genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel-associated box in human synovial sarcoma.";

EMBO J. 14:2333-2340(1995).
                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
| sarcoma, X breakpoint 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Synovial sarcoma;
                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                          TISSUENCE FROM N.A. (ISOFORM 2).

TISSUE-Skin;

MEDLINE-2388257; PubMed=1247932;

A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Rapleton M.J., Usdin T.B., Tocshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Broark S.A., McKarnan K.J., Malek J.A., Gunarathe P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Florer ation and initial malysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRAB-ŘELATED.
K -> KHPWRQVCDRGIHLVNLSPFWKVGREPASSIKALLC
                                                                                                                                                                                                                                                                Gure A.O., Tuereci O., Sahin U., Tsang S., Scanlan M.J., Jager E., Knuth A., Pfreundschuh M., Old L.J., Chen Y.-T.;
"SSX: a multigene family with several members transcribed in normal Lestis and human cancer." Int. J. Cancer 72:965-971(1997).
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001909; KRAB.
InterPro; IPR001909; KRAB.
Pfam; PF01352; KRAB; 1.
SMART; SM00349; KRAB; 1.
PROSITE; PS50806; KRAB RELATED; 1.
Multigene family; Transcription regulation; Alternative splicing.
DOMAIN
20 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Could act as a modulator of transcription.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=060225-2; Sequence=VSP_006274;
NOTC=No experimental confirmation available;
-!- SIMILARITY: Belongs to the SSX family.
-!- SIMILARITY: Contains 1 KRAB-related domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=060225-1; Sequence=Displayed;
                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98021352; PubMed=9378559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC016640; AAH16640.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U90842; AAC05821.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew, HGNC:11339; SSX5.
MIM; 300327; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
33
                                                                                   SSX5 protein.
SSX5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGAGCCAGCAGGAGGAAGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LeuGlyPheLysValThrLeuProProProPheMetCysAsnLysGlnAlaThrAspPheGln 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAsnGlyAspAspThrPheAlaLysArgProArgAspAspAlaLysAlaSerGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysTyrSerGluLysIleSerTyrValTyrMetLysArgAsnTyrLysAlaMetThrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgSerLysAlaPheAspAspIleAlaThrTyrPheSerLysLysGluTrpLysLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                                                                                                                                                                                     KRAB-RELATED.
BREAKPOINT FOR TRANSLOCATION TO FORM THE SSXT-SSX1 FUSION PROTEIN (RARE).
BREAKPOINT FOR TRANSLOCATION TO FORM THE SSXT-SSX1 FUSION PROTEIN.
E440D1B2AE34E9F7 CRC64;
                                                        MIM; 312820; --
GO; GO: 000534; C:nucleus; TAS.
GO; GO: 0003714; E:transcription co-repressor activity; TAS.
InterPro; IPR001909; KRAB.
InterPro; IPR003655; KRAB. related.
Ffam; PF01352; KRAB; 1.
SWART; SM0049; KRAB; 1.
PROSITE; PS50806; KRAB. RELATED; 1.
Chromosomal translocation; Proto-oncogene; Multigene family;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-975-856-1 (1-576) x SSX1_HUMAN (1-188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGACCCTGAGGAAGATGACGAG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAspProGluGluAspAspGlu 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                              21931 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              8.968-70
784.00
84.04%
79.26%
EMBL; S79325; AAB35378.1;
                  PIR, S55057, S55057.
Genew; HGNC:11335; SSX1.
MIM; 312820; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                    111
                                                                                                                                                                                                                                                                                                                                                                              188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                                                                                                                                                62
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SSX5_HUMAN
ID SSX5_HUMAN
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Pred. No.:
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SEQUENCE

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DOMAIN

Query Match: DB:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R MIN; 314939'; C:nucleus; NAS.

R GO; GO:000367; F:DNA binding; NAS.

R GO; GO:000367; F:DNA binding; NAS.

R GO; GO:000635; P:regulation of transcription, DNA-dependent; NAS.

R GO; GO:000635; P:regulation of transcription, DNA-dependent; NAS.

R InterPro; IPR001909; KRAB;

R InterPro; IPR001909; KRAB;

R InterPro; IPR001909; RAB;

R Pfam; PF01352; KRAB; 1.

R Pfam; PF01352; KRAB; 1.

R Pfam; PF00006; zf-CZHz, sub.

R PRNTS; PR000046; zrrKFINER.

R RNART; SM00349; KRAB; 1.

R SNART; SM00355; ZRF CZHz; 3.

R R PROSITE; PS00028; ZRTC FINGER.

R PROSITE; PS00028; ZRNC FINGER. CZHZ 1; 5.

R PROSITE; PS0157; ZLNC FINGER. CZHZ 2; 5.

M TRANSCRIPC; PS0157; ZLNC FINGER. CZHZ 2; 5.

M Nuclear protein; Repeat.

M Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 TTCGATGATATTGCCAAATACTTCTCTAAGAAAGAGGGGAAAAGATGAAATCCTCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AAAATCGTCTAT---GTGTATATGAAGCTAAACTATGAGGTCATGACTAAACTAGGTTTC
                                                                                                                     SEQUENCE OF 139-289 FROM N.A.
SEQUENCE OF 139-289 FROM N.A.
BRAINO M., Archidiacono N., Franze N., Rosati M., Rocchi M.,
Ballabio A., Grimaldi G.,
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in transcriptional regulation.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-PINGER PROTEINS.
Patrosso C., Frattini A., Lucchini F., Repetto M., Sacco M.G., Zoppe M., Vezzoni P., and a constant of the KRAB zinc finger gene subfamily mapped in YACs 1 Mb telomeric of HPRT."; denomics 18:223-229(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 KRAB domain.
-!- SIMILARITY: Contains 5 C2H2-type zinc fingers.
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CZHZ-TYPE 1.
CZHZ-TYPE 2.
CZHZ-TYPE 3.
CZHZ-TYPE 4.
CZHZ-TYPE 4.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-975-856-1 (1-576) x ZN75_HUMAN (1-289)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S67970; AAB29696.1; -. EMBL; X68010; CAA48147.1; -.
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113.50
42.25%
26.06%
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HSSP, P25490, 1ZNM.
Genew, HGNC:13145; ZNF75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 ProSerGlyLysLeuAsnThrSerGluLysValAsnLysThrSerGlyProLysArgGly 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATCCTCGGAGAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GlyasnaspPheaspasnaspProasnargGlyasnGlnValGluHisProGlnMetThr
                                                                                                                                                                                                                                                                                                                                                                                  21 MetGlnLysAlaPheAspAspIleAlaLysTyrPheSerGlnLysGluTrpGluLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LeuGlyPheLysAlaThrLeuProProPheMetArgAsnLysArgValAlaAspPheGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||
| AsnAspSerLysGlyValProGluAlaSerGlyProGlnAsnAsnGlyLysGlnLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTTATGAAGAATC
                                                                                                                                                                                                                                                                                                                                                     ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Lung fibroblast;
MEDLINE=94116987; PubMed=8288223;
Villa A., Zucchi I., Pilia G., Strina D., Susani L., Morali
            GRGEAR (in isoform 2).
/FTId=VSP 006274.
P -> Q (IN REF. 2).
AD2A3096931C5E37 CRC64;
                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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P51815; HUMAN
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 75.
                                                                                                                                                                                                                                                                                                          US-09-975-856-1 (1-576) x SSX5_HUMAN (1-188)
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                                                                                                                                              2.23e-69
780.00
85.11%
77.66%
                                                                             AA;
                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                             Alignment Scores:
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OB:
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., More T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Josares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., Mordwan P.J., McKernan K.J., Malek J.A., Glubes R.A.,
A Willalon D.K., Wuzny D.M., Sodergren B.J., Lux, Glubes R.A.,
A Pahoy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Botherzhon and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                  408
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|21 AlaThrCysLysGlnGluLeuProLysLeuMetAspLeuHisGlyLysGlyProThrGly 140
                                              AAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCACGGGAATGAT, 249
                                                                                                                                                                                                                                                                                                                                                               101 AspThrHisSerValGlnLysTrpHisArgAlaPheProArgLysLysArgLysLysPro 120
                                                                                            9
                                                                                                                                                                                61 ThrGlyAsnAspHisProlleSerValSerThrSerGluIleGlnThrSerGlyCysGlu 80
LysThrLeuTyrAsnAspValMetGlnAspIleTyrGluThrValIleSerLeuGlyLeu 55
                                                                                                                                                                                                                                                            81 ValSerLysLysThrArgMetLysIleAlaGlnLysThrMetGlyArgGluAsnProGly
                                                                                                                                                                                                                                                                                                                        -----AGCCTCCAG----AGAATCTTCCCGAAGATCATGCCCAAGAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                             349 GCAGAGGAAGAAATGGTTTGAAGGAAGTGCCAGAGGCCATCTGGCCCACAAAATGATGGG
                                                                                                                                                                                                                              265 ---AACCACAGGAATCAGGTTGAACGTCCTCAGATGACTTTCGGC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21883946; PubMed=11779858; Conrcy A.T., Sharma M., Holtz A.E., Wu C., Sun Z., Weigel R.J.; Conrcy A.T., Sharma M., Holtz A.E., Wu C., Sun Z., Weigel R.J.; "A novel zinc finger transcription factor with two isoforms that are differentially repressed by estrogen receptor-alpha."; J. Biol. Chem. 277:9326-9334(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBTDIT, QBTDIS, QPDEN, QBUDNE, 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
Zinc finger protein 398 (Zinc finger DNA binding protein p52/p71).
ZNF398 OR ZERG OR KIAA1339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Bemis G., Langston Y., Tucci S.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     250 TTTGGTAACGATCGA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642 AA
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                                                                                         56 LysLeuLys----
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           MEDIINE=20181126; PLOM N.A.
MEDIINE=20181126; PLOMPGd=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Neddiction of the coding sequences of unidentified human genes. XVI.
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
For large proteins in vitro.";
-!- FUNCTION: Function as a transcriptional activator.
-!- SUBCELLUAR LOCATION:
-!- SUBCELLUAR LOCATION:
-!- ALTERNATIVE PRODUCTS:
--- BVECH-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 KFAB domain.
-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:18373; ZNF398.

GO; GO:0005634; C:nucleus; NAS.

GO; GO:0016563; F:transcriptional activator activity; NAS.

GO:0006355; P:transcription of transcription, DNA-dependent; NAS.

InterPro; IPR001909; KRAB.
                                                                                                                                                                                                                                       Name=2; Synonyms=p52;
Isold=08TDJ7-2; Sequence=VSP_006926;
-1-INDUCTION: By estrogen receptor alpha.
-1-SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PSS0805, ZH. CARAB, 1.
PROSITE; PSS0805, ZH. CARAB, 1.
PROSITE; PSS0157, ZHOC FINGER C2H2_1; 7.
PROSITE; PSS0157, ZHOC FINGER C2H2_1; 7.
PROSITE; PSS01157, ZHOCF ACTIVATOR; DNA-binding; Zhnc-finger; Metal-binding; Nuclear protein; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isororm 2).
/FTIG=VSP 006926,
; 69AA38FCD84FF633 CRC64;
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31
21
41
Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                          Name=1; Synonyms=p71;
IsoId=Q8TD17-1; Sequence=Displayed;
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C2H2-TYPE
C2H2-TYPE
C2H2-TYPE.
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C2H2-TYPE.
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C2H2-TYPE.
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EMBL; AC004890; AAA5824.1; ALT_SEQ.
EMBL; BC043295; AA443295.1; -.
EMBL; AB037760; BAA925577.1; -.
TRANSFAC; T05129; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01352; KRAB; 1.
Pfam; PF00096; zf-C2H2; 8.
ProDom, PD000003; zf-C2H2; 2.
SMART; SM00349; KRAB; 1.
SWART; SM00355; ZnF_C2H2; 8.
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VARSPLIC
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ZN_FING
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-------ileProThrAspProSerGlu 220
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| GluPro---Gly11eSerThrSerAsp11eLeuSerTrp11eLysGlnGluGluGluPro 239
                                                                                                                                                     AAGTTACGAAAGGCCTTCGATGATATTTGCCAAATACTTCTCTAAGAAAAGAGTGGGAAAAG 117
                                                                                                                                                                                                                                                                             118 ATGAAATCCTCGGAGAAAATCGTCTATGTG---TATATGAAGCTAAACTATGAGGTCATG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleSerMetAspTyrAlaIleAsnGlnProAspValLeuSerGlnIleGlnProGluGly 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 TTCCACGGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 ATGACTTTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and characterization of a KRAB-containing zinc finger protein, ZNFB17, and its isoforms.", Biophys. Res. Commun. 288:771-779[2001].
--- FUNCTION: May function as a transcription factor. May play an important role in erythroid maturation and lymphoid proliferation.
--- SUBCELUIAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                 LysValProValAlaPheAspAspValSerIleTyrPheSerThrProGluTrpGluLys
                                                                                                                                                                                                                                                                                                                                                                                                     175 ACTAAACTAGGTTTCAAGGTCACCTCCCAACTTTCATGCGTAGTAAACGGGCTGCAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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BEDLINE-1247764; PubMed=11688974;
Takeshima H., Nishio H., Wakao H., Nishio M., Koizumi K., Oda A.,
Koike T., Sawada Ki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
SIMILARITY: Contains 1 KRAB domain.
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   32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z317_HUMAN STANDARD; PRT; 595 AA. Q96PQ6; Q96PM0; Q96PT2; 28-FBB-2003 (Rel. 41, Created) 10-PEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 2inc finger protein 317.
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Indels:
Gaps:
                                                                                             US-09-975-856-1 (1-576) x Z398_HUMAN (1-642)
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240 GlnValGlyAlaPro 244
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9.85%
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Query Match:
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          It is produced through a collaboration of new atics and the EMBL outstation -
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119 GluargGlyalaHisGlnGlyAlaCysAlaAspTrpGluThrProSerLysThrLysTrp 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AAAATCGTCTATGTGTATATGAAGCTA---AACTATGAGGTCATGACTAAACTAGGTTTC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 AAGGTCACCCTCCCACCTTTCATG---CGTAGTAAACGGGCTGCAGACTTCCACGGGAAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AGCCTC-----CAGAGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGAGAGGAAGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50805; KRAB, 1.
PROSITE; PS50805; KRAB, 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
PROSITE; PS50187; ZINC_FINGER_C2H2_2; 13.
Transcription regulation; Zinc-finger; Metal-binding; Nuclear protein;
DNA-binding; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 TTCGATGATATTTGCCAAATACTTCTCTAAGAAGAGGGGAAAAGATGAAATCCTCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ArglysleuTyrLysAspValMetLeuGluAsnTyrSerAsnLeuThrSerLeuGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATITITICGIAACGATCGAAACCACAGGAATCAGGTIGAACGTCCTCAGATGACTTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform 3 and lecture. /FIId=VSP 006915. Missing (in isoform 1 and isoform 3). /FIId=VSP 006916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TId=VSP 006916.
9AFF574ZA34EE859 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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C222 - TYPE.

C222 - TYPE.
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                                                                                                                                                                                                           EMBL; AF275255; AAL29188 1; EMBL; AF148135; AAL29182.1; EMBL; AF307096; AAL29190.1; EMBL; AF307097; AAL29191.1; PIR; UC7779; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67941 MW;
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94.00
47.62%
30.48%
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Best Local Similari
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ZN_FING
ZN_FING
VARSPLIC
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
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PK3G R4 070173 PK3G_RAT RESULT

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| Se GingingiyginSerGiyThrGiuHisCysAsnTyrTyrVal-------Glu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             490 AGGCATGTTTCCCCCTTTTGGGTCCAGATGTCTTGTTAATCTTCTCCAAGGTACTTGGAT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 LeuProPheGlyLysAlaSerAla-----IleGlyPheAsnProAlaValLeuPro 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 GGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGGTTTCGATCGT---TAC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAGGTGGGAGGGTGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 TTCCCGGGGGGCACAGCTGTTTCCCATCATTTTGTGGGCCAGATGCCTCTGGCACTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAACCATTTTCTTCCTCTGCTGGCTTCTTGGGCATGATCTTCGGGAAGATTCTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGluAspProArgPheSerAlaLeuThrProSerSerThrGlyLeuAspLysCysHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lattard V., Longin-Sauvageon C., Lachuer J., Buronfosse T., Benoit E. "Cloning, sequencing and tissue dependent expression of FMO1 and FMO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dimethylaniline monooxygenase [N-oxide forming] 1 (EC 1.14.13.8)
(Hepatic flavin-containing monooxygenase 1) (FMO 1) (Dimethylaniline oxidase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rmol.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTTGAAACCTAGTTTAGTCATGACCTCATAGTTTAGCTTCATATACA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 ProGluAsnAsnVal -----ProHisHisTyrSerProTyrSer 182
                                                                                                                                                                                                                          PX.
C2 DOMAIN.
MW: SED4C2239968C4B2 CRC64;
                                                                                                                                                                                                                                                                                                                                          1505
133
16
17
17
5
              SWART; SWO312; PX; 1.
SWART; SWO312; PX; 1.
PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
PROSITE; PS00915; P13_4 KINASE_1; 1.
PROSITE; PS00916; P13_4 KINASE_2; 1.
PROSITE; PS00916; P13_4 KINASE_2; 1.
PROSITE; PS5029; P13_4 KINASE_3; 1.
R PROSITE; PS5029; P13_4 KINASE_3; 1.
R TIAIRFERSE; Kinase; Membrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                  1402 1499 C2 I
1505 AA; 170974 MW;
                                                                                                                                                                                                                                                                                                                                          0.95
89.50
42.24%
28.45%
8.89%
         SM00146; PI3Kc; 1.
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                                                                                                                                                                                                                             1371
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                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the dog."
                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE-Regenerating liver;

MEDLINE-98104888; PubMed=9516481;

OND F., Nakagawa T., Saito S., Owada Y., Sakagami H., Goto K.,

Suzuki M., Matsuno S., Kondo H.;

A novel class II phosphoinositide 3.kinase predominantly expressed in

the liver and its enhanced expression during liver regeneration.";

J. Biol. Chem. 273:7731-7736(1998).

-!- FUNCTION. IN VITRO, PHOSPHORYLATES PIDINS AND PIDINS4P BUT NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUDINS (4,5) P2.

-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-1D-myo-inositol 4-phosphate dyl-1D-myo-inositol 4-phosphate dyl-1D-myo-inositol 4-phosphate - ADP + 1-phosphatidy1-1D-myo-inositol 3-d-bisphosphate.
-!- SUBCELLULAR LOCATION: Membrane-associated (By similarity)
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN NORMAL LIVER. HIGH LEVELS ALSO FOUND IN REGENERATING LIVER. VERY LOW LEVELS FOUND IN PROPER LIVER.
-!- DEVELOPMENTAL STAGE: HIGHER LEVELS OF EXPRESSION FOUND IN ADULT LIVER THAN IN FETAL LIVER.
-!- SIMILARITY: Contains 1 C2 domain.
-!- SIMILARITY: Contains 1 D2 domain.
-!- SIMILARITY: Contains 1 phox homology (PX) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                                                                                                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing polypeptide (EC 2.7.1.154) (Phosphoinositide 3-kinase-C2-gamma) (PtdIns-3-kinase C2 gamma) (P13K-C2gamma).
                                                                                                                                                                                                       1505 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR0008938; ARM.
Interpro; IPR000008; ARM.
Interpro; IPR0000093; C2.
Interpro; IPR000403; PI3 PI4 kinase.
Interpro; IPR000403; PI3 R C2.
Interpro; IPR000341; PI3K C2.
Interpro; IPR001263; PI3Ka.
Interpro; IPR001263; PI3Ka.
PEAM: PF00168; C2; 1.
PEAM: PF00168; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ffam, F70-00, 72, 14 kinase, 1. Pfam, PF00454; P13K_C2; 1. Pfam, PF00792; P13K_C2; 1. Pfam, PF00794; P13K_bd; 1. Pfam; PF00794; P13Ka; 1. SMART; SM00239; C2; 2. SMART; SM00142; P13K_C2; 1. SMART; SM00144; P13K_C2; 1. SMART; SM00145; P13K_i; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB009636; BAA25634.1; -.
                                                                    361 AATGGTTTGAAGGAA 375
                                                                                                             159 AladiyieuGlydiu 163
                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                       STANDARD;
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CENTRAINCESTED. (4): TISSUER. 17. (150FORM 2).

STRAINCESTED. (4): TISSUER. 17. (150FORM 2).

MEDLINE=22354683; PubMed=12466851;

A OKAZAKI Y. FULTON M., KRAIKAWA T., Adachi J., Bono H., Kondo S.,

Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Radarelii R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelii R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Bradt D., Hrokawa N., Jackson I.E., Cousins S.,

Balake J.A., Bradt D., Hirokawa N., Jackson I.J., Jarvis E.D.,

A Dalla E., Darapain T.A., Fletcher C.F., Forrest A., Gough J.,

A Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

A Kawaji H., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

A Konagaya A., Kawaji I., Marchionni L., McKenzie L., Miki H.,

A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

A Maglott D.R., Maltais L., Pontius J.U., Oli D., Ramachandran S.,

Betrovsky N., Pillai R., Pontius J.U., Oli D., Ramachandran S.,

Bandelin A., Schneider C., Semple C.A., Sectou M., Sang I., Yang L.,

Nilming L.G., Wymahaw-Boris A., Yanagisawa M., Yang I.,

Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

A Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N.,

A Hara A., Hashikawa T., Konno H., Nakamura M., Sakazume N.,

A Yasunishih A., Yoshiho W., Imocani K., Ishii Y., Itoh M., Kagawa I.,

A Yasunishih A., Yoshiho M., Waterston R., Lander E.S., Rogers J.,

Panawa Yasanishiho W., Panagisaka Y.,

Bananishi A., Yoshiho M., Waterston R., Lander E.S., Rogers J.,

Panawa Yasanishiho W., Panayanishino W., Panagisaki Y.,

Panawa Yasanishiho W., Panagisaki Y.,

Panawa Yasanishiho W., Panagisaki P.,

Panawa Yasanishiho W., Panagisaki P.,

Panawa Yasanishiho W., Panagisaki P.,

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MEDLINE=2238825; PubMed=12477922;

RIGURE R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Parange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Anvillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., M., Mahiling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ahrithing M., Madan J.W., Green E.D., Dickson M.C., Rothiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Human and mouse cDNA sequences.";
           10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RalBP1 associated Eps domain containing protein 1 (RalBP1-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation 60,770~{\rm full-length~cDNAs."};
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
TISSUE=Muscle;
TISSUE=Muscle;
TISSUE=Muscle;
TISSUE Muscle;
TISSUE Muscl
                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 447-743 FROM N.A. (ISOFORM 1).
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Biol. Chem. 272:31230-31234(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 8-743 FROM N.A.
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                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                 protein 1).
               HERE REPARED TO THE PROPERTY OF THE PROPERTY O
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 ACTOGROATCTTCCTCAGGGTCGCTGATCTCTTCATAAACCACCAGCTGCTTTCTCTCAC 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 CCTCTGGCACTTCCTTCAAACCATTTTCTTCCTCTGCTGGCTTCTTGGGCATGATCTTCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 GGAAGAITCTCTGGAGGCTGCCGAAAGTCAICTGAGGACGTTCAACCTGATTCCTGTGGT 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 CCAAGGIACTIGGATTICCCGGGGGGCACAGCIGTTICCCATCATTITGTGGGCCAGATG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 -----TyrSerAspPhePro-------PheProGluAspTyr 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------ArgPheSerLeuLeuLysCysIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 eArgPheLysThrLysValCysLysValThrLysCysProAspPheThrValThrGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00419; ADXEDTASE.
PRINTS; PR00368; FADENR.
PRINTS; PR00370; FMOXYGENASE.
Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ------ValSerAsnSerCysLysGluMetSerCys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multigene family, Acetylation.

S SIMILARITY.

ACETYLATION (BY SIMILARITY).

A 1 FAD (ADP PART) (POTENTIAL).

NADP (POTENTIAL).

AA, 59927 MM, 9F3458484540521F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
dimethylaniline N-oxide + NADP(+) + H(2)O.
-!- COFACTOR: FAD (By similarity).
-!- SUBCELLULAR LOCATION: Microsomal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743 A.A.
                                                                                                                  -!- TISSUE SPECIFICITY: Liver.
-!- SIMILARITY: Belongs to the FMO family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF384053; AAK97433.1; -.
InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001327; PAD_pyr_redox.
InterPro; IPR000960; Flav_cont_mnoxgn.
Pfam; PP00743; PMO-like; I.
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REP1 MOUSE
1D REP1 MOUSE STANDARD;
1C CO4916; Q8C9J9; Q99LR8;
DT 10-OCT-2003 (Rel. 42, Created)
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123 nTrpGlu 125
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Best Local Similarity:
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INIT_MET
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MOD_RES
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NP_BIND
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NP_BIND
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DB:
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315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 HisThr-TrpArgLysHisSerArgHis-----ProSerGlyGlyAsnSerGluArgPr 141
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59 ArgLeuAlaAlaSerTyrSerSerAspSerGluAsnGlnGlySerTyrSerGlyVallle
                                                                                                                                                                                                                                                                                                                                                                                39 AsnThrValLysAspLeuProLeuProArgPheValAlaSerLysAsnGluGlnGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90343821; PubMed=2383273;
Guan S.H., Falick A.M., Cashman J.R.;
"N-terminus determination: FAD and NADP binding domain mapping of hog
liver flavin-containing monooxyganase by tandem mass spectrometry.";
Biochem. Biophys. Res. Commun. 170:937-943(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                           223 CGGGCTGCAGGCTTCCACGGGAATGATTTTGGTAACGATCGAAACCAC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 ------AGGAATCAGGTTGAACGTCCTCAGATGACTTTCGGCAGCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 GTGCCAGAGGCATCTGGCCCACAAATGATGGGAAACAGCTGTGCCCCCCCGGGAAATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 AGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGAAACATG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 27, Last sequence update)
Dimethylaniline monooxygenase [N-oxide forming] 1 (EC 1.14.13.8)
(Heparic flavin-containing monooxygenase 1) (FWO 1) (Dimethylaniline oxidase 1).
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NEDLINE=90212556; PubMed=2322534;
Gasser R., Tynes R.E., Lawton M.P., Korsmeyer K.K., Ziegler D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartlodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                           190 ----AAGGTCACCCTCCCACCTTTCATGCGTAGTAA----
                                                                                                                                                                                                         151 ATGAAGCTAAACTATGAGGTCATGACTAAACTAGGTTTC------
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                                     US-09-975-856-1 (1-576) x REP1_MOUSE (1-743)
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                                                                                                                                              11 TyrpheGlyArgSerGlnPhe---
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Biochemistry 29:119-124(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REMEL; AF031939; AAB99436.1; -.
REMEL; AF041967; BAC31117.1; ALT_INIT.
REMEL; AF041967; BAC31117.1; ALT_INIT.
REMEL; AF041967; BAH02266.1; ALT_FRAME.
REMEL; T09179; T09173.
REMEL; BC02268; EF-hand.
REMEL; REPERO; IPR0002648; EF-hand.
RICE-PRO; IPR0002648; EF-hand.
REMEL; REMO0267; EH; I.
REMEL; PS00018; EF-HAND; 1.
REMOSITE; PS00018; EF-HAND; 1.
REMEL; PS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: Expressed in all tissues examined. The highest level expression was found in the kidney and testis.
-!- PTM: EGF stimulates phosphorylation on Tyr-residues.
-!- SIMILARITY: Contains I EH domain.
-!- SIMILARITY: Contains I EF-hand calcium-binding domain.
-!- AUTION: Ref. 3 sequence differs from that shown due to a frameshift in position 719.
                                                                                                                                                                                                                                                                                   SUBGUIT: Homodimer (Presential). Interacts with RALBPI, CRK and GRB2. Binding to RALBPI does not affect its Ral-binding activity. Forms a complex with the SH3 domains of CRK and GRB2 which may link it to an EGF-responsive tyrosine kinase.

ALTERNATIVE PRODUCTS:
EVENT.Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLED COLL (POTENTIAL).
PHOSPHOKYLATION (POTENTIAL).
PHOSPHOKYLATION (POTENTIAL).
VEXTERESESSOFULTOPENTIARADEDTAIVHPV ->
VEXTELLEISLFTGRSFKODRFTAGYLQYAHTP (in
                                                                                MEDLINE=21285759; PubMed=11389591;
Kim S., Cullis D.N., Feig. L.A., Baleja J.D.;
Kim S., Cullis D.N., Feig. L.A., Baleja J.D.;
"Solution structure of the Repal EH domain and characterization of its binding to NPF target sequences.";
Biochemistry 40:6776-67385(2001).
-!- FUNCTION: May coordinate the cellular actions of activated EGF receptors and Ral-GTPases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=054916-2; Sequence=VSP_007956, VSP_007957; Note=Due to intron retention. No experimental confirmation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=vSP 007956.
Missing (In isoform 2).
/FTId=vSP 007957.
25510DII254CF4A6 CRC64;
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INTERACTION WITH RALBPI.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                          STRUCTURE BY NMR OF 227-318
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Best Local Similarity:
Query Match:
DB:
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CTISSUE=Brain, and Lymph;

XX Straubborg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Astraubborg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Redusher R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Halsch F.,

Bromstein M.J., Usdin T.B., Peterse G.J., Abramson R.D., Mullahy S.J.,

Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., Loquellano N.A., Peterse G.J., Abramson R.D., Mullahy S.J.,

Bromstein M.J., Wofkernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., McEwan P.J., McKettman K.J., Malek J.A., Gubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabes J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Chnerchion and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                385 CCTCTGGCACTTCCTTCAAACCATTTTCTTCCTCTGCTGGCTTCTTGGGCATGATCTTCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
Mao Y., Xie Y., Yie Y., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,
Tang R., Chen X., Wu C.,
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    Q96D71; QBNDR7; QBWG62; Q9BXY9;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RalBP1 associated Eps domain containing protein 1 (RalBP1-interacting protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bloecker H., Boecher M., Brandt P., Mewes H.-W., Weil B., Wiemann S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: May coordinate the cellular actions of activated EGF receptors and Ral-Grpases (By similarity)
-!-SUBUNIT: Homodimer (Potential). Interacts with RALBPI, CRK and GRB2. Binding to RALBPI does not affect its Ral-binding activity. Forms a complex with the SH3 domains of CRK and GRB2 which may link it to an EGF-responsive tyrosine kinase (By similarity).
                                                                                                                                                                                                                                                              265 ITCGATCGTTACCAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAG
                                                                                                                             325 GGAAGATTCTCTGGAGGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
                                      Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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123 nTrpAsp 125
                                                                                                                                                                                                                                                                                                                                                                                               205 GTGGGAG 199
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REP1 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 ACTOGNOANCTICCTCAGGGNCGCTGATCTCTTCATAAACCACCAGCTGCTTTCTCTCAC 506
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------ValSerAsnSerCysLysGluMetSerCys-----°
                                                                  Wu R.-F., Ichikawa Y.;
"An essential lysyl residue (Lys208) in the substrate-binding site of:
portoine FAD-containing monooxygenase.";
Eur. J. Biochem. 229:749-753(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             늉
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem. Res. Toxicol. 11:1145-1153(1998).

-!- FUNCTION: This protein is involved in the oxidative metabolism a variety of xenobiotics such as drugs and pesticides.

-!- CATALYTIC ACTIVITY: N,N cimethylaniline + NADPH + O(2) = N,N-dimethylaniline N-oxide + NADP(+) + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR00159; Adrndx_reductase.
InterPro; IPR00137; FAD_pyr_redox.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001327; FAD_pyr_redox.
Pfam; PF00143; FM0-like; I.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00316; FMDXYGENASE.
PRINTS; PR00316; FMDXYGENASE.
Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Microsome; INT_MET 0 0 ACETYLATION.
MOD RES 0 ACETYLATION.
NP_BIND 8 13 FAD (ADP PART) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                         "N-glycosylation of pig flavin-containing monooxygenase form 1: determination of the site of protein modification by mass \,
                                                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITE.
MEDLINE-90451545; PubMed-9778310;
Korsmeyer K.K., Guan S., Yang Z.C., Falick A.M., Ziegler D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLATION.
FAD (ADP PART) (POTENTIAL)
NADP (POTENTIAL)
SUBSTRATE BINDING.
N-LINKED (GLCNAC. . ) (HIC
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Microsomal.
-!- TISSUE SPECIFICITY: Liver.
-!- SIMILARITY: Belongs to the FWO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
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   TISSUE=Liver;
MEDLINE=95278229; PubMed=7758472;
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207
207
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531 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: FAD
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                                                                                                                                                                                                                                                                                                                             Cashman J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  spectrometry
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Pred. No.:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     450
                                                                                                                                                                                  ---CAGATGACTTTCGGCAGCCTCCAGAGAATCTTCCCGAAG 330
                                                                                                                                                                                                                                                                                         391 GGCCCACAAAATGATGGGAAACAGCTGTGCCCCCGGGAAATCCAAGTACCTTGGAGAAG
                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                        79 ProProProProGlyArgGlydinValLysLysGlySerValSerHis-----AspThr
                                                                                                                                            Mech. Dev. 49:23-36(1995).

-! FUNCTION: May function as switches in neuronal development.
-! FUNCTION: May function.
-! STUBELLULAR LOCATION: Nuclear.
-! TISSUE SPECIFICITY: Low level expression is seen in undifferentiated proliferating cells of neural epithelium. A greater expression is seen in the maturing neurons after they leave the neural epithelium. It is also found in the gut epithelium and adrenal medulla.
-! SIMILARITY: Contains I HMG box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECURINCE FROM N.A.

TISSUE=Embryo;

MEDLINE=95267693; PubMed=7748786;

Wannogho D., Rex M., Cartwright E.J., Pearl G., Healy C.,

Scotting P.J., Sharpe P.T.;

"Embryonic expression of the chicken Sox2, Sox3 and Sox11 genes
suggests an interactive role in neuronal development.";

Mech. Dev. 49:23-36(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P48436; ISX9.
InterPro; IPR000910; HMG 12_box.
Pfam, PF00505; HMG box; I.
SMART, SM00399; HMG 1.
PROSITE; PS50118; HMG BOX 2; 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  451 ATTAACAAGACATCTGGACCCAAAAGGGGGAAACATG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transcription factor SOX-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-ALA.
POLY-GLU.
POLY-PRO.
POLY-ARG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U12534; AAB09664.1; -. PIR; I50707; IS0707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
       283 GAACGTCCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 ACCC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 yPro 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P48435
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SX11 CHICK
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                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||
11 TyrPheGlyArgSerGInPhe-----Tyr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: |||
19 IleAlaLeuLysLeuValAlaValAlaGlnSerGlyPheProLeuArgValGluSerlle 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::: ||||||| |||::: ||||||| 39 AsnThrValLysAspLeuProLeuProArgPheValAlaSerLysAsnGluGlnGluSer 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 ArgHisAlaAlaSerTyrSerSerAspSerGluAsnGlnGlySerTyrSerGlyValIle 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF251052; AAK34942.1; --
R EMBL; BC012764; AAH12764.1; --
R EMBL; BC021211; AAH1271.1; --
R EMBL; BC021211; AAH1271.1: --
R EMBL; BC0021211; AAH1271.1: --
R EMBL; AL831300; CAD38569.1; --
R InterPro; IPR000261; ERF91.
R InterPro; IPR000261; ERF15.homology.
R InterPro; IPR000361; EFF10.
R PR0017F; PS00037; EH; 1.
R PR0517F; PS00031; EH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTTCTCTAAGAAGAGTGGGAAAAGATGAAATCCTCGGAGAAAATCGTCTATGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH RALBP1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH -> FP (IN REF. 2; AAH12764).
1DFF29711DB2B5E4 CRC64;
                                                                                                                                     IsoId=Q96D71-3; Sequence=VSP_007955;
PTM: EGF stimulates phosphorylation on Tyr-residues (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 -----AAGGTCACCCTCCCACCTTTCATGCGTAGTAA----
                                                                                                                                                                                                                                               SIMILARITY: Contains 1 EH domain.
SIMILARITY: Contains 1 EF-hand calcium-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL). PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 2).

FTIG=VSP 007953.

Missing (in isoform 2).

FTIG=VSP 007954.

Missing (in isoform 3).

FTIG=VSP 007955.

A - V (IN REF. 1).

V -> I (IN REF. 3).
                                                                    IsoId=096D71-2; Sequence=VSP_007953, VSP_007954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF-HAND (POTENTIAL).
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Matches:
Conservative:
Mismatches:
Indels:
   IsoId=Q96D71-1; Sequence=Displayed;
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80769 h
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38.89%
24.07%
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742
744 AA;
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Best Local Similarity:
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                                      Name=2
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CA BIND
DOMAIN
DOMAIN
MOD RES
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CONFLICT
SEQUENCE
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EMBL; BC011887; AAH11887.1; ALT INIT.

EMBL; BC013603; AAH13603.1; ALT_INIT.

EMBL; X60123; CAS94195.1; -.

EMBL; X52356; CAA36582.1; -.
   MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
MEDLINE-88247738; PubMed-3380682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 252-446 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 340-395 FROM N.A.
                                                                                                                                                                                                                                                                       SEQUENCE OF 1-250 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-387 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Biol. 2:363-374(1990).
                                                                                                                                                                                                                                                                                    TISSUE=Teratocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thiesen H.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells
   114
                                                                                                                                                                                                                                                                                                                                                                                                                                           337 CCCAAGAAGCCAGCAGAAGAAAATGGTTTGAAGGAAGTGCCAGAGAGGCATCTGGCCCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 CAAAATGATGGGAAACAGCTGTGCCCCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 GlyGlyGlySerLysSerAlaLysSerSerGlyLysLysCysSerLysLeuLysAlaAla 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: ||| ::: |||
184 GluTyrValPheGlyAlaLeuLysValSerSerLysAlaValLysCysValPheValAsp 203
                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                             115 AAGATGAAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------AGACTGCGTGAGAAAGCAGCTGGTGGTTTAT 531
                                                                                                                                              AGGAGACCCAGGGATGATGCTCAAATATCAGAGAGGTTA-----CGAAAGGCCTTCGAT 78
                                                                                                                                                           :::||||||
LysArgProMetAsnAlaPheMetValTrpSerLysIleGluArgArgLysIleMetGlu
                                                                                                                                                                                                           -----ProArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GATATTGCCAAATACTTCTCTAAGAAAGAGTGGGAA
                                                                                                                                                                                                                                                                                                                                           ---AAACGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATCGAAACCACAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                            277 CAGGITGAACGICCICAGAIGACIIITCGGCAGCCICCAGAGAAICTICCCGAAGAICAIG
                                                                                                                                                                                                                                                                     MetLeuLysAspSerGluLys1le-----
                                                                                                                                                                                                                                                                                                                  175 ACTAAACTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZN38 HUMAN STANDARD, PRT, 446 AA.
P17036; P13683; Q9NXXB; Q9NXXI; Q9UC15; Q9UC16;
O1-APR-1990 (Rel. 14, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
26-CT-2003 (Rel. 42, Last annotation update)
The finger protein 38 (Zinc finger protein KOX25) (Zinc finger protein He.12) (Zinc finger protein 3) (HZF3.1 protein).
ZNF38 OR KOXZ5 OR ZNF3.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457 AAGACATCTGGACCCAAAAGGGGGAAACATGCCTGGACCCAC-----
 8E4B0A457F8BA833 CRC64;
                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGAGATCAGCGACCCTGAGGAAGATGACGAG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 GluGluGluGluAspGluGluAspGlu 214
                                                                                                                    US-09-975-856-1 (1-576) x SX11_CHICK (1-396)
 43503 MW;
                                   1.49
86.50
31.75%
21.33%
8.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Ovary, and Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 661
396 AA;
                                                                       Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                          Percent Similarity:
Best Local Similari
                       Alignment Scores:
Pred. No.:
                                                                                                                                                                    20
                                                                                                                                                                                             79
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SEQUENCE
                                                                                Query Match:
DB:
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2N38 HUM
2N3 PLU
2N3 PLU
DDT 201-
DDE ZIN
DDE ZIN
OCS HOM
OCS MARN (1)
RRN (1)
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Altaubberg R.L., Feinged E.A., Grouse L.H., Derge J.G.,
Altaubberg R.L., Feinged E.A., Grouse L.H., Derge J.G.,
Altaubberg R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
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"Isolation of cDNAs encoding finger proteins and measurement of the
"Isolation of cDNAs levels during myeloid terminal differentiation.";

Corresponding mRNA levels during myeloid terminal differentiation.";

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-! FUNCTION: INVOLVED IN CELL DIFFERENTIATION AND/OR PROLIFERATION.

-! SUBCELLULAR LOCATION: Nuclear (Potential).

-! SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92051312; PubMed-1945843; Rosati M., Marino M., Franze A., Tramontano A., Grimaldi G.; "Members of the zinc finger protein gene family sharing a conserved N-terminal module.";
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Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isoquen S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 19:5661-5667(1991).
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MEDLINE=91145339; PubMed=2288909;
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CAR2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
L -> P [IN REP. 2].
GEKPY -> IRDSG (IN REF. 5).
GEKPYECNECGKAFSGSSHLYQHORIHTGEKPYECMECGGK
FTYSGALYQHO. -> FALPFYTLIRLLPSYOPIYTNBAAF
FTYSGALYHPALIVRLECVHSIAMPKKV (IN REF. 3).
W; 67A6926807304782 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 ACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGAACTTCCACGGGAATGATTTTGGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 AACGAICGAAACCACAGG------AATCAGGTTGAACGTCCTCAGATGACTTTC 303
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90 LeuAspArgGluThrArgThrGluAsnAspGlnGluIleSerGluAspThrArgSerHis 109
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EMBL, X07290; CAA30269.1; -. PIR, S00754; S00754. Genew, HGNC:13104; ZNP3. Genew, HGNC:13089; ZNF3.
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349 GCAGAGGAAGAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGG 408
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Straubberg R.;
Straubberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC002818; AAH02818.1; -
GO, GO:0005822; C:intracellular; IEA.
GO, GO:0003675; F:nucleic acid binding; IEA.
GO, GO:000355; F:rucleic acid binding; IEA.
InterPro; IPR001909; RNAB.
InterPro; IPR003555; RNAB.
PF01352; KRAB; 1.
SMO0349; KRAB; 1.
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Q8C964
Q8TPS6
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Q8BV16
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Q9BU88
           Q9bu88 homo sapien
                                                                                                                                                                                   March 31, 2004, 13:40:37; Search time 47 Seconds (without alignments) 7733.553 Million cell updates/sec
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1 ATGAACGGAGACGCCTT.....ATGACGAGTAACTCCCCTCG
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                  protein search, using frame_plus_n2p model
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Fgapext
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sp_bacteria:*
sp_fungi:*
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sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
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                                                                                                              DNA-dependent; IEA.
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Eukarycia, Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OTC-2003 (TrEMBLrel. 25, Last annotation update)
DJ54B20.1.1 (Novel SSX family protein (Isoform 1)) (Fragment).
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                                                                                                                                                                             PROSITE, PSSO806; KRAB RELATED; 1.
SEQUENCE 170 AA; 19457 MW; D981F807A9C7EAB1 CRC64;
                                                                                                                                                                                                                                     1170
1170
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                                       Strausberg R.,
Strausberg R.,
Submitted (APR-2001) to the EMBL/GenBank/DDBJ data
EMBL, BC005904; AAH05904.1;
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003676; F:intcleic acid binding; IEA.
GO; GO:000375; F:intcleic acid binding; IEA.
InterPro; IPR001909; RRAB.
InterPro; IPR001855; RRAB.
Fine: FF01352; KRAB; I.
SMART; SM00349; KRAB; 1.
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636.00
82.05%
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                SEQUENCE FROM N.A. TISSUE=Bone marrow;
                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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SEQUENCE FROM N.A.
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Q96Q11,
01-DEC-2001 (
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01-UTM-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Synovial sarcoma, X breakpoint 3.
Homo sapiens (Human)
Homo sapiens (Human)
Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGA----
 KRAB RELATED; 1.
; 25173 MW; 2BF8E1FFA4D58094 CRC64;
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1137
111
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                                                     Length:
Matches:
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                                                   1.15e-62
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220 uAsnSerTrp 223
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              AA;
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Best Local Similarity:
Query Match:
DB:
PROSITE; PS50806;
SEQUENCE 223 AA;
                                       Alignment Scores:
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101 LysLeuGlyPheAsnValThrLeuSerLeuPheMetArgAsnLysArgAlaThrAspSer 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 ACTITICGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGCAGAAAA
                                                                                                                                                                                                                                                                                                                           1 ATGAACGGAGACGACGTTTGCAAGGAGACCCCAGGGATGATGCTCAAATATCCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                               21 ArgSerLysHisProTrpArgGlnValCysAspLeuAlaLeuHisLeuValThrLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ProPheTrpLysValGlyArgGluProAlaSerIleThrGluAlaLeuLeuCysGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AAACTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAAACGGGCTGCAGACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005676; F:nucleic acid binding; IEA.
GO; GO:0006355; F:nucleic acid binding; IEA.
InterPro; IPR001909; KRAB:
InterPro; IPR001909; KRAB.
InterPro; IPR003555; KRAB.
InterPro; IPR003555; KRAB.
InterPro; IPR00355; KRAB; I.
PROMINE; SM00349; KRAB; I.
PROMINE; PS50806; KRAB.
RELATED; I.
ROW TER.
196 AA; 22299 MW; 71CAIDELEGING.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SYT-SSX protein (Fragment).
Homo sapiens (Human).
Eukaryte; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                  61 TTACGAAAG-------
                                                                                                                                                                                              4.59e-48
545.50
63.78%
57.65%
53.22%
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                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                  Alignment Scores:
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Q9Y444;
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AC 093
DT 011-
DT 011-
DE SYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 ArgAsnAspSerAspAsnAspArgAsnArgGlyAsnGluValGluArgProGlnMetThr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::
121 SerAspSerLysGlyValProGluAlaSerGlyProGlnAsnAspGlyLysLysLeuCys 140
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                                                                                                                                                                                                                                                                                                                                                                       1 ATGAACGGACGACGCCTTTGCAAGGACCCAGGGATGATGCTCAAATATCAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                     Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; Z98304; CAC41946.1; -

EMBL; Z98304; CAC41946.1; -

EMBL; Z98304; CAC41946.1; -

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005625; F:nuclation of transcription, DNA-dependent; IEA.

InterPro; IPRO01909; KRAB.

InterPro; IPRO01909; KRAB.related.

Pfam; PF01552; KRAB; 1.

SMART; SM00349; KRAB; 1.

MON TUPE: PS08066; KRAB RELATED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96Q10 PRELIMINARY; PRT; 196 AA.
Q96Q10,
G1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ54B20.1.2 (Novel SSX family protein (Isoform 2)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465
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SEQUENCE FROM N.A.
Grafham D.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCCGGGAAATCCAAGTACCTTGGAGAGATTAACAAGACATCT
                                                                                                                                                                                06EC7C89D35A1A30 CRC64;
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1113
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                    155 155
155 AA; 17689 MW;
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576.00
80.65%
72.90%
56.20%
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Stred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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SEQUENCE
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                         342
                                                                                                                            GAIGGGAAACAGCIGIGCCCCCCCCGGGAAAICCAAGIACCTIGGAGAAGAITAACAAGACA 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||:::::: |||||||
41 IleHisGluArgSerGlyAsnArgGluAlaGluLysGluGluArgArgGlyThrAla 60
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                                               20
                                        1 GluArgProGlnMetThrPheGlyArgLeuGlnGlyIleSerProLys1leMetProLys
                                                                                             21 IysproAlaGluGluGlyAsnAspSerGluGluValProGluAlaSerGlyProGlnAsn
                                                                                                                                            41 AspGlyLysGluLeuCysProProGlyLysProThrThrSerGluLysIleHisGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 GGCCCACAAAATGATGGGAAACAGCTGTGCCCCCCGGGAAATCCAAGTACCTTGGAGAAG
                         GAACGTCCTCAGATGACTTTCGGCAGCCTCCAGAGAATCTTCCCCGAAGATCATGCCCAAG
                                                                           343 AAGCCAGCAGAAGAAGAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HisArgTrpSerSerGlnAsnThrHisAsnIleGlyArgPheSerLeuSerThrSerMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20210694; PubMed=10749136; MEDLINE=20210694; PubMed=10749136; dos Santos N.R., Torensma R., de Vries T.J., Schreurs M.W.J., dos Bruijn D.R.H., Kater-Baats E., Ruiter D.J., Adema G.J., van Muijen G.N.P., Geurts van Kessel A.; Heterogeneous expression of the SSX cancer/Lestis antigens in melanoma lesions and cell lines."; Cancer Res. 60:1654-1662(2000).

EMBL; AF190791; AAF44724.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AA; 12399 MW; 981EBD852BA31DF8 CRC64;
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52
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                            113 AA
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                                                                                                                                                                                                                                                            PRT;
 US-09-975-856-1 (1-576) x Q8WWZ9 (1-64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.29e-17
247.50
50.88%
45.61%
24.15%
                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, SSX2 (Fragment).
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                                                                                                                                                                                 463 TCTGGACCCAAA 474
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                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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Best Local Similarity:
Query Match:
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                         283
                                                                                                                              403
                                                                                                                                                                                                                                                                           Q9NZK4;
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                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCGTGAGAGAAAGCAGCTGGTGTTTATGAAGAGATCAGCGACCCTGAGGAAGATGAC 561
                                                                                                                                                                                                                                                                                                                  SYT and SSX, involved in the t(X;18) in human synovial sarcoma.";
                                                                                                                                                                                                                                                                                                   38 GluAlaSerGlyProGlnAsnAspGlyLysGluLeuCysProFroGlyLysProThrThr
                                                                                                                                                                                                                                                                                                                                                     382 GAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGCCCCCCCGGGAAATCCAAGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homos sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                Gill S., Shipley J., Chan A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
04-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BA564H18.1 (Synovial sarcoma, X breakpoint 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whitehead S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AL596242; CAD18884.1; -.
NON TER 64 64
SEQUENCE 64 AA; 7014 MW; 43ADB72AF2FB9613 CRC64;
                                                                                                                                          98 AA; 11136 MW; 1C71F5C8D54513DD CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                MEDLINE=55038836; Pubmed=7951320; Clark J., Rocques P.J., Crew A.J., Gusterson B.A., Cooper C.S.; "Identification of a novel genes, SY (P11.2;q11.2) translocation found in Nat. Genet. 7:502-508 (1994).
EMBL, X79200; CAB36970.1; -.
NON TER 1 1.136 MW; IC71F50
                                                                                                                                                                                                                                                                       US-09-975-856-1 (1-576) x Q9Y444 (1-98)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.93e-18
255.00
84.38%
75.00%
24.88%
                                                                                                                                                                               4.56e-29
363.00
91.36%
80.25%
35.41%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
DB:
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAG 564
 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                        442
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Q8WWZ9
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RRA RRA
RRT RRA
SO ET
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86 ValtyrMetLysArgAsnTyrileArgMetThrAspLeuGlyValThrValAsnGlnPro 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 CCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATCGA 264
                                                                                                                                                                                                                                                                                                                                                                                                 The FAND CONDECTION.

The FAND CONDECTION CONDECTION TO THE FAND COND Phase I & II Team;

The RAILYSIS of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";

IN ALURE 420:563-573 (2002).

R EMBL; AKO76879; BAC36519.1; -..

R GO; GO:0005622; C:intracellular; IEA.

R GO; GO:0005625; F:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001909; RRAB.

R InterPro; IPR003655; RRAB.

R InterPro; IPR03555; RRAB.

R PRO; SOSOS (RRAB.)

R PRO; IFE PRO; SOSOS (RRAB.)

R PRO; IFE PRO; PRO; RRAB.)

R PRO; IFE PRO; PRO; RRAB.)

R PRO; IFE PRO; PRO; RRAB.)

R PRO; IFE PRO; PRO; RRAB.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 CGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATCAGCGACCCTGAGGAAGATGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AGGAGACCCAGGGATGATGCTCAAATATCAGAGGTTACGAAAGGCCTTCGATGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 GCCAAATACTICTCTAAGAAGAGIGGGAAAAGAIGAAATCCTCGGAGAAAATCGTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 GIGIAIAIGAAGCIAAACIAIGAGGICAIGACIAAACIAGGIITICAAGGICACCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                12.7M.R.-2003 (TrEMBLrel. 23, Created)
01.7M.R.-2003 (TrEMBLrel. 23, Last sequence update)
01.0T.-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical KRAB box/KRAB-related containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             il protein.
165 Aa; 19584 MW; 5FE61134DD87BAC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                                                                                      165
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-975-856-1 (1-576) x Q8C5Z3 (1-165)
                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AspLysGlnSerLeuvalGlu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.57e-13
214.50
45.00%
31.11%
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium,
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                      Q8C5Z3;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAAATACTTCTCTAAGAAAGAGGGGAAAAGATGAAATCCTCGGAGAAAATCGTCTAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 CCTITCATGCGTAGTAAACGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATCGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 AACCACAGGAATCAGGTTGAACGTCCTCAGATGACTTTCGGCAGCCTCCAGAGAATCTTC 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValTyrMetLysArgAsnTyr1leArgMetThrAspLeuGlyValThrValAsnGlnPro 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GlyLysGluGln 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AGGAGACCCAGGGATGATGCTCAAATATCAGAGAAGTTACGAAAGGCCTTCGATGATATT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::: :: |||||||| :::||||||| SerThrTyrPheSerAspGludIvpGlyLysLeuThrGlnTrpGlnLysSerAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------diyile---GluvalHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 GCATCTGGCCCACAAAATGATGGGAAACAGCTGTGCCCCCCGGGGAAATCCAAGTACCTTG
                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-dependent; IEA
                                                                                                                                                                                                                                                                                                                                   Strausberg R., Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SMO349; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50806; KRAB RELATED; 1.
SEQUENCE 128 AA; 15290 WW; F88614D1CBFF3B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0707-2003 (TrEMBLrel. 24, Created)
01-0707-2003 (TrEMBLrel. 24, Last sequence update)
01-070-2003 (TrEMBLrel. 25, Last annotation update)
Similar to TKEN CDNA 4930414C09 gene.
Mus musculus (Mouse).
                                   100 nMetProGlyProThrAspCysValArgGluAsnSerTrp
                 CATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,5e-13
214.50
45.00%
31.11%
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                             NCBI_TaxiD=10090;
                                                                                                                                                                                                                                                                                                                      TISSUE=Testicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 Ser--
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                 184
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DB:
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                                                           67 AAGGCCTTCGATATTGCCAAATACTTCTCTAAGAAAGAGTGGGAAAAGATGAAATCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                    238 CACGGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ThrserValThr1leSerPheHisAsnValGluGlySerLeuAlaSerGlyGluAsnAsp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 TGCCCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 ---ValAsnValTrpSerHisArgLeuArgGluArgLysTyrArgValIleTyrSerGlu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CAG 294
                                                                                                                                                                                                                                                                                                         187 TTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGAC------TTC 237
                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| ::: ||| ::: ||| | :::: ||| | :::: ||| | :::: ||| | :::: ||| | :::: ||| | :::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: || | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | :: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: ||| | ::: || | ::: ||| | ::: ||| | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: || | :: 
                                                                                                23 LysAlaPheGlnAspIleSerThrTyrPheSerAspGluGluTrpGlyLysLeuThrGln 42
                                                                                                                                                                                                                             :::|||
43 TrpGlnLysSerAlaTyrValTyrMetLysArgAsnTyr1leArgMetThrAspLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 ACTITICGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGCAGAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 GAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAACAGCTG
                                                                                                                                                                                  127 TCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAACTAGGT
                                                                                                                                                                                                                                                                                                                                                                     63 ValThrvalAsnGlnProvalPheMetArgGlyLysGluGlnAlaLysGlnSerLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 GGGAAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAG
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCT---
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34
8
16
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Last annotation update)
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 ATCAGCGACCCTGAGGAAGATGACGAG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 IleSerAspThrGluGluGluGluAsp 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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(1-170)
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160.50
64.62%
52.31%
15.66%
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08,
23,
   US-09-975-856-1 (1-576) x Q9CPU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Sonobe H., Takeuchi T.;
"SSX-HSTT.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 Cys-----
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Best Local Similarity:
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SSX-HSTT.
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SIGUINCE FROM N.A.

SIGUINCE FROM N.A.

SIGUINCE TOTALSUBE-TESTIS;

KAWAI J., Shinagawa A., Shibara K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Shibara K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Shibara K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Shibara K., Yoshino M., Pukuda S.,

A Arakawa T., Jamanaka I.,

A Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Kadora K., Masuda H.A., Ashburner M., Batalov S., Casavant T.,

A Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Watuni R., Younita M., Wagner L., Washio T.,

B Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

B Blake J., Boli C., Fletcher C., Fujita M., Garibodi M.,

Gustincich S., Hill D., Hofmann M., Hume D., Kamiya M., Lee N.H.

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

B Suzuki H., Toyo-oka K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

A Havashizaki W.,

A Havashizaki W., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                 --Glylle---GluValHisAsp 126
                                                                                                                                                                                  445 GAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGAAACATGCCTGGACCCCACAGACTG 504
                                                                                                                                                                                                                                              ------AspGluThrSerGlyIleArg-----ValAsnValTrpSerHisArgLeu 142
                                                                                                                                                                                                                                                                                                                CGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATCAGCGACCCTGAGGAAGATGACGAG 564
                                                              385 GCATCTGGCCCACAAAATGATGGGAAACAGCTGTGCCCCCCGGGAAATCCAAGTACCTTG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AKO15135; BAB29722.1; -.
EMBL; AKO6218; BAB24465.1; -.
BEMBL; AKO6218; BAB24465.1; -.
MGD; MGI:191523; 493041041; EA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:000355; F:mulleic acid binding; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001309; KRAB.
InterPro; IPR003655; KRAB_related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F63F702B7FDF7227 CRC64;
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828
87
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87
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Last annotation update)
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Conservative:
Mismatches:
Indels:
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PROSITE; PS50806; KRAB RELATED;
SEQUENCE 170 AA; 19636 MW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0TN-2001 (TrEMBLrel, 17, 01-0TN-2001 (TrEMBLrel, 17, 01-0CT-2003 (TrEMBLrel, 25, 4930414C09R1k, protein.
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211.50
47.34%
34.32%
20.63%
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SMART; SM00349; KRAB;
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127 Ser-----
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Percent Similarity:
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Pred. No.:
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EMBL; AY138489; AAN39531.1;

NON_TER 1 1

10NN_TER 39

SEQÜENCE 39 AA; 4336 MW;
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Query Match:
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Best Local Similarity:
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Pred. No.:
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SEQUENCE
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                                                                                                                                                                                                                                 88 GluGlyAsnAspSerGluGluValProGluAlaSerGlyProGlnAsnAspGlyLysGlu 107
                                                                               295 ATGACTTTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGCAGAAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlnGlnTyrGlyGlyTyrArgProThrGlnProGlyProProGlnProProGlnGln 72
                                                                                                                                                  73 ArgProTyrGly------TyrAspGlnileMetProLysLysProAlaGlu 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammālia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Y.,
Nilsson G., Larsson O.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY138488; AAN39530.1; -.

NON_TER 39

NON_TER 39

SEQUENCE 39 AA, 4336 MW; 8FC179F66C8C7E0D CRC64;
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Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie
Nilsson G., Larsson O.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 GAGGCATCTGGCCCACAAATGATGGGAAACAGCTGTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 GluAlaSerGlyProGlnAsnAspGlyLysGluLeuCys 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SS18/SSX2 fusion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBIZG9;
01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
SSI8/SSX2 fusion protein (Fragment).
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                               CTGTGCCCCCCGGGA 429
                                                                                                                                                                                                                                                                                                                                                                                                                          108 LeuCysProProGly 112
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137.00
87.88%
75.76%
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                               415
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0812H0
10 Q81ZH0
DT 01-MADDT 01-MADDT 01-MADDT 01-MADDT 01-MADDT 01-MADDT 01-MADDT 00 MADDT 
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10812G9
10812G9
10012G
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322 TICCCGAAGAICAIGCCCAAGAAGCCAGCAGGAAGAAAAIGGITIGAAGGAAGIGCCA 381
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                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                       382 GAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 GAGGCATCTGGCCCACAAATGATGGGAAACAGCTGTGC 420
8FC179F66C8C7E0D CRC64;
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6 0
                                                                                                                                                                                                                                                                                         27 GluAlaSerGlyProGlnAsnAspGlyLysGluLeuCys 39
                                                                                                                                                                                                                                                                                                                                                                    Q81ZG8 PRELIMINARY; PRT; 39 AA.
Q81ZG8;
Q1CG8;
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
SS18/SSXZ fusion protein (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SSI8/SSX2 fusion protein (Fragment)
SSI8/SSX2 FUSION
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Indels:
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Thu Apr

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GE Homo sapiens (Human).

CE EMERYORA; MELEZOA; Chordata; Craniata; Vertebrata; Euteleostomi;

CE MAMMALIA; Euthbria; Primates; Catarrhini; Hominidae; Homo.

CE NUCBI_TAXID=9606;

RN [1]

RP Mei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Y.,

RA Nilsson G., Larsson O.; the EMBL/GenBank/DDBJ databases.

RE SEQUENCE FROM N.A.

RA Nilsson G., Larsson O.; Larsson C., Dwight T., Xie Y.,

RA Nilsson G., Larsson O.; Larsson C., Dwight T., Xie Y.,

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RA NILSSON G., Larsson G.; La
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Search completed: March 31, 2004, 13:59:50 Job time : 50 secs

Title: Perfect score:

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Scoring table:

Searched:

Database

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Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

I (bases 1 to 979)

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BM471266 AGENCOURT
BQ432374 AGENCOURT
BQ432374 AGENCOURT
BQ432374 AGENCOURT
BQ432374 AGENCOURT
BG231752 AGENCOURT
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BEB10396 601303658
BC229064 AGENCOURT
BC333981 6012435310
BEB1039 601201423
BC478295 601201423
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        ACCESSION
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
BM806411
          BM806411 AGENCOURT
BU194624 AGENCOURT
BU161779 AGENCOURT
BQ222907 AGENCOURT
                                                                                                                                  March 31, 2004, 15:16:19; Search time 2745 Seconds (without alignments) 6266.162 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                              US-09-975-856-1
576
1 ATGAACGAAGACGACGCTT.....ATGACGAGTAACTCCCCTCG 576
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                                                                                                                                                                                                                                                                                                                                                                                       55026578
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BU194624
BU161779
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                                                                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seg length: 200000000
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Match Length DB
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Best Local Si
Matches 525;
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                           ö
                                                                               /tissue_type="melanotic melanoma"
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/clone_lib="NIH_MGC_72"
/nohe="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                124
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 836)
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                                                                                                                                                                                                                                                                                                ATGAACGGAGGACGACGCCTTTGCAAGGAGCCCACGGTTGGTGCTCAAATACCAGAGAAG
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                                                                                                                                                                                                                                                                    1 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAG
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                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                Length 979;
                                                                                                                                                                                                                                         49; Indels
                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                             86.2%; Score 496.6; DB 12;
91.5%; Pred. No. 1.8e-131;
ive 0; Mismatches 49;
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Homo
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AGENCOURT 7969283 NIH_MGC_72
5', mENA Sequence.
BU194624.1 GI:22708608
   location/Qualifiers
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Homo sapiens
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//organism="Homo sapiens"
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/nore="Organism: skin; Vector: pGMV-SPORT6; Site_1: Not1;
/norage insert size 2 kb. Library constructed by Life
Technologies." ô 240 373 133 120 180 300 360 433 420 493 480 553 540 193 253 313 613 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI3525 row: f column: 16

High quallity sequence stop: 624. 9 1 ATGAACGGAGACGACGCCTTTGCAAGGAGCCCCAGGGATGATGCTCAAATATCAGAAG 134 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGGTGGGAAAAAGATG AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAAACTATGAGGTCATGACTAAAA 194 AAAGCCTCAGAGAAATCTTCTATGTGTATGAAGAAAGTATGAGGCTATGACTAAA CTAGGITTCAAGGICACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 254 cragerircaageccacereceaecrircargreraraaaeggecgaagacriecag 241 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 314 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT 301 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAAGAA AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAAACAGCTGTGC 434 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGAGCTGTGC 421 CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 494 CCCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAGATCTGGACCCAAAAGGGGG 481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAATC 554 GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC Gaps ô ch 85.9%; Score 495; DB 13; Length 8 il Similarity 91.3%; Pred. No. 4.9e-131; 525; Conservative 0; Mismatches 50; Indels

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AGENCOURT 7675894 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6095680 5', mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov
Tissue Procurement: ATCC/CDTD/prp
Tissue Procurement: ATCC/CDTD/prp
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LibMil368 row: h column: 17
High quality sequence stop: 625.
High quality sequence stop: 625.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 863)
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/mol type="mRNA"
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Technologies."
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                                                                      481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
                                              CCCCCGGGAAATCCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAGGGGG
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Sybrange insert size 2 kb. Library constructed by Life
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 887)
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Tissue Procurement: ATC/DOTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 22
High quality sequence stop: 739.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases; 1 to 781)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llhl.gov

Plate: LLAM13509 row: n column: 08

High quality sequence stop: 634.

Incetinn/Qualifiers

Incetinn/Qualifiers
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AGENCOURT 7896851 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6159943
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                                                                                            78 argaacceaceaceacecerriecaaesaececaceerresaecricaaeraccaeaeas
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/lab_host="DH10B (phage-resistant)"
/clone_lb="NHH MGC_72"
/note="Organ: Skin, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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NH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.B. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov.i column: 22
High quality sequence start: 258
High quality sequence stop: 436.
Location/Qualifiers
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                                      GTTTCAAGGCCACCTCCCACCTTTCATGTTAAAACGGGCCGAAGACTTCCAGGGA
                                                                               ATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACTTTCG
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/db_xref="taxon:9606"
/clone="IMAGE:5563101"
  GITICAAGGICACCCICCCACCIT
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                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC/DCT/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1304 row: g column: 11
High quality sequence stop: 696.
Location/Qualifiers
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89.8%; Pred. No. 3.6e-127;
ive 0; Mismatches 59;
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                                /mol_vope=manusconspress
/mol_vope=manusconspress
/db xref==taxcn:9606"
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/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/clone_lib="Ntluo phage-resistant"
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/clone_lib="Ntluo phage-resistant"
/clone="Organ: skin, Vector: pcMV-SPORT6; Site_1: Not1;
/verage insert size 2 kb. Library constructed by Life
Technologies.
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Pred. No. 3.4e-
0; Mismatches
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5', mRNA SEQUENCE.
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Homo sapiens
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Matches 517; Conserv
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1. (Dases 1 to 1135)

In Illa MC http://mgc.nci.nih.gov/.

In National Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM8415 row, o column: 07

High quality sequence stop: 650.
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                                                                   499 cccccaggaaaagcaaaharrrcrcaggaagarraaraagagarcrcgacccaaaaggg
                                                                                                                                                   AAACATGCCTGGACCCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
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83.2%; Score 479.2; DB 10; Length
Best Local Similarity 89.9%; Pred. No. 2e-126;
Matches 514; Conservative 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                  541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG 576
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 888)
Math-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LILNL at:
Plate: LimM13530 row: j column: 22
High quality sequence stop: 636.
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                                                                                            AĞENCOURI 7859139 NIH_MC
5', mRNA Sequence.
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BQ432374.1 GI:21171450
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B. (Dases 1 to 950)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, inc.
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.7550845 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6066127
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/mol type="mRNR"
/db xref=taxon:9606"
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/lab_fost=="roplop"
/lab_fost="roplop"
/lone lib="logodin1"
/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: Not!; The library was contributed by The Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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                                                                                                                                                         TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGAAGCCAGCAGAGGAAGAA
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                                                                                                                                                                                                                                                                                                                                                              CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
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                                                           GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                         GGGAATGATTTTGATAATGACCATAACCGCAGGATTCAGGTTGAACATCCTCAGATGACT
                                                                                                                                                                                                                                                                361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAAACAGCTGTGC
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Pred. No. 2.2e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim, Y.S.

21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Sorea Research Viscong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCGACCCTGAGGAAGATGACGAGTAACTCCC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 AGCGACCCTGAGGAAGATGACGAGTAACTCCC 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: F column: 07
High quality sequence stop: 602.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB158955.1 GI:28145081
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91.1%;
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CB158955
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Best Local Similarity
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COMMENT
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AUTHORS
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkcvits, M.D., Ph.D.
cDNA Library Preparation: Miklos Placovits, M.D., Ph.D.
cDNA Library Preparation: Miklos I Brownstein (NHGRI), Shiraki
roshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://inage.llnl.gov.e column: 09
High quality sequence stop: 790.
High quality sequence stop: 790.

1. 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this
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// Ab_xref="taxon:9606" |
// Ab_orf="inkage." | Mod. 97" |
// Ab host="inkage." |
// Ab host=
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                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
Strausberg, Ph.D.
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Best Local Si
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="lmAdR:6066127"
/tissue_type="melanotic melanoma"
/tish host="PhiloB (phage-resistant)"
/clone_lib="The MGC 72"
/note="Torgan: Skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                Score 470.8; DB 13;
Pred. No. 4.8e-124;
0; Mismatches 57;
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89.9%;
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516; Conservative
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Best Local S:
Matches 516
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Contact: Robert Strausberg, Ph.D.
Email: agapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM338 row: d column: 15
High quality sequence stop: 571.
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                                                524 GAJACATGCCTGGACCCACAGACTGCGTGAAGAAAGCAGCAGCGGGGGATTTATGAAGAGA
               AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAAACAGCTGTGC
                                                                                                                               CCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCCAAAA-GGGG
                                                                                                                                                                                         GAAACATGCCTGGACCCCACAGACTGCGTGAGAAAGCAGCTGGTGG-TTTATGAAGAGA
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/mol_type="mRNA"
/db_xref="texcon:9606"
/db_xref="texcon:9606"
/clone="texcon:9608"
/lab_host="bH10B (phago-resistant)"
/clone lib="NIH MG-72"
/note="Organ: %Kin; Vector: pCMV-SpORT6; Site 1: NotI;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Plate: LLAM13297 row: g column: 17
High quality sequence stop: 483.
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Pred. No. 3.3e-117;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

El (bases it to 867)

In (bases it to 867)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov/

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Location/Qualifiers

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High quality sequence stop: 641.

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| Adamy750 row: j column: 26 |

| Adamy750 row: j column: 27 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 72"
/once="organ: skin, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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      AGAAGCAAGGCCTTTGATGATGATTGCCACATACTTCTCTAAGAAAAAGAGTGGAAAAAGAGTG 178
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                                                               AAATCCTCGGAGAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
                                                                                                                                                                                                                                                                                               GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
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BE891434.1 GI:10350764
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BE891434
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                                                                                                  1 ATGAACGGAGACGACGCCTTTGCAAGGAGCCCAGGGATGATGCTCAAATATCAGAAG
                                                    2
  Length 867;
  DB 10;
                                                    56;
Score 423.4; DB 10
Pred. No. 1.9e-110;
0; Mismatches 56;
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